FIGURE 1

Human DNase I

```
LOCUS
                         1039 bp
                                    mRNA
                                                               06-MAR-1995
            HUMDNASEI
                                                     PRI
DEFINITION
            Human DNase I mRNA, complete cds.
            M55983
ACCESSION
            M55983.1
VERSION
                      GI:181623
KEYWORDS
            DNase I.
            Human pancreus, cDNA to mRNA.
SOURCE
  ORGANISM
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
               (bases 1 to 1039)
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
            91067672
  MEDLINE
                     Location/Qualifiers
FEATURES
                     1..1039
     source
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                     /db xref="taxon:9606"
                     /clone="hDNase-18-1"
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     sig peptide
                     160..225
                     /gene="DNase I"
                     160..1008
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                     LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
                     DAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLI
                     PDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDHYP
                     160..1008
     gene
                     /gene="DNase I"
     mat peptide
                     226..1005
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BASE COUNT
                226 a
                         305 c
                                  282 q
                                           226 t
ORIGIN
        1 tcctgcacag gcagtgcctt gaagtgcttc ttcagagacc tttcttcata gactactttt
       61 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag
      121 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg
      181 ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgcagcc
      241 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
      301 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg
      361 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
      421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
      481 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg
      541 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc
      601 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac
      661 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg
      721 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc
      781 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca
      841 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgccgtt
      901 gttescgact eggetettee etttaaette eaggetgeet atggeetgag tgaccaactg
      961 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc
     1021 cacaccagtt qaactgcag
//
```

```
LOCUS
            MHDNASE.DN
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                                    mRNA
                                                     PRI
                                                               06-MAR-1995
            Human DNase I mRNA, complete cds, Mature sequence modified to remove Narl site
DEFINITION
ACCESSION
            M55983
NID
            g181623
KEYWORDS
            DNase I.
SOURCE
            Human pancreus, cDNA to mRNA.
  ORGANISM
            Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Komo.
REFERENCE
               (bases 1 to 1039)
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
            91067672
  MEDLINE
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                     PCGNOTFNREPAIVRFFSRFIEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKKGL
                     EDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAG
                     MLLRGAVVFDSALEFNEQAAYGLSDQLAQAISDHYPV&VMIK*
     deue
                     160. .1008
                     /gene="DNase I"
     mat_peptide
                     226. .1005
                     /gene="DNase I"
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BASE COUNT
                         236 c
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       61 CTCGTCAGCT ACATIGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
      121 AGAGACAGCC ACCTGACTGC CGTGGGGGAAC CTGCTGGACA ACCTCAATCA GGACGCACCA
      181 GACACCTATC ACTACGTGCT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
      241 CIGITCGIGI ACAGGCCIGA CCAGGIGTCT GCGGIGGACA GCIACIACIA CGAIGAIGGC
      301 TGCGAGCCCT GCGGGAACGA CACCTTCANC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
      361 CGGTTCACAG AGGTCAGGGA GITTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
      421 GTAGCCGAGA TCGACGCTCI CIATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
      481 GAGGACGICA IGTIGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
      541 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
      601 GACACCACAG CTACACCCAC GCACTGTGCC TAIGACAGGA TCGTGGTTGC AGGGATGCTG
      661 CICCGAGGGG CCGITGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
      721 CIGAGIGACC AACIGGCCCA AGCCATCAGI GACCACTATC CAGIGGAGGI GAIGCIGAAG
      781 TGA
11
```

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858 BP SS-DNA
                                                    SYN
                                                               29-AUG-2000
LOCUS
            PAS155 GB.
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
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                     <10..>75
     frag
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                     <10...>75
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                     /db xref="taxon:9606"
                     /clone="hDNase-18-1"
                     /tissue type="pancreas [Split]"
                     10..75
     sig_peptide
                      /gene="DNase I"
                     10..>75
     CDS
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                      /codon start="1"
                      /product="DNase I"
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                      D... [Split]"
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                      76..858
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                      /note="1 to 72 of 104linker"
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      frag
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                      join(76..>126,<127..>129,<131..147)
      frag
                      /note="1 to 78 of 102linker [Split]"
                 177 A 260 C 251 G 170 T 0 OTHER
 LASE COUNT
 ORIGIN
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        61 CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC AGACATTTGG GGAGACCAAG
       121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC
       181 CTGGTCCAGG AGGTCAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC
       241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC
       301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC
       361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT
       421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTTG CCATTGTTCC CCTGCATGCG
       481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA
       541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT
       601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG
       661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG
       721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACTTC
       781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG
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841 GAGGTGATGC TGAAGTGA

LOCUS

HMFGLLC2.D

(A) pAS6 - light chain

721 bp

```
DEFINITION HUMANISED HMFG1 LIGHT CHAIN VNp LEADER.
ACCESSION .
KEYWORDS
SOURCE
  ORGANISM
REFERENCE
            1 (BASES 1 TO 342)
  AUTHORS
            VERHOEYEN ET AL
            CONSTRUCTION OF RESHAPED HMFG1 ETC
  TITLE
  JOURNAL
            IMMUNOL. (1993):78, 364-370
            SCANNED IN FROM JOURNAL
COMMENT
FEATURES
  SITES
This is the sequence of the HMFG1 light chain gene with the
Vnp leader sequence attached. Translate from
residue 1. Note residue 399 is T > A in all clones leading
to R133 silent mutation (T in Verhoeyen paper)
BASE COUNT
                197 a
                                  162 g
                         202 c
                                            140 t
ORIGIN
                 7
                          LEADER SEQ
      1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCGAC
       61 ATCCAGATGA CCCAGAGCCC AAGCAGCCTG AGCGCCAGCG TGGGTGACAG AGTGACCATC
      121 ACCTGTAAGT CCAGTCAGAG CCTTTTATAT AGTAGCAATC AAAAGATCTA CTTGGCCTGG
      181 TACCAGCAGA AGCCAGGTAA GGCTCCAAAG CTGCTGATCT ACTGGGCATC CACTAGGGAA
      241 TCTGGTGTGC CAAGCAGATT CAGCGGTAGC GGTAGCGGTA CCGACTTCAC CTTCACCATC
      301 AGCAGCCTCC AGCCAGACGA CATCGCCACC TACTACTGCC AGCAATATTA TAGATATCCT
      361 CGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAACGAA CTGTGGCTGC ACCATCTGTC
      421 TICATCTICC CGCCATCTGA IGAGCAGTIG AAATCIGGAA CIGCCTCTGI TGTGTGCCTG
      481 CIGAATAACI ICTAICCCAG AGAGGCCAAA GIACAGIGGA AGGIGGAIAA CGCCCICCAA
      541 TCGGGTAACT CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
      601 AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA CGCCTGCGAA
      661 GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAGAGCT TCAACAGGGG AGAGTGTTAG
      721 A
11
```

DNA

4/113

Figure 3(B)

```
SYN
                                                              29-AUG-2000
                          730 BP SS-DNA
            HHMFG1KLC
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
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                     10..730
     frag
                     /note="1 to 72 of 104linker"
                     join(10..>63,<65..81)
     frag
                     /note="1 to 72 of 103linker [Split]"
                     join(10..>60,<61..>63,<65..81)
     frag
                     /note="1 to 78 of 102linker [Split]"
                                  184 G
                                           140 T
                                                      0 OTHER
FISE COUNT
                198 A
                         208 C
FIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
      121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC
      181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC
      241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTC AGCGGTAGCG GTAGCGGTAC CGACTTCACC
      301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
      361 AGATATCCTC GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
      421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
      481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
      541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
      601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
      661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
      721 GAGTGTTAGA
```

Figure 3 (c)

HMFG-1 light chain with Vnp Leader (shaded)

MGWSCILFLVATATGVHSDIQMTQSPSSLSASVGDRVTITCKSSQSL LYSSNQKIYLAWYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGT DFTFTISSLQPEDIATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC

(0) PAS6 - heavy drain

```
HHMFGIHC.D
LOCU$
                        1404 bp
                                   DNA
DEFINITION
           HUMANISED HMFG1 heavy chain
ACCESSION
         · HHMEGIA
KEYWORDS
SOURCE
  ORGANISM
REFERENCE
  AUTHORS
           VERHOEYEN BT AL
  TITLE
           CONSTRUCTION OF RESHAPED HMFG1 etc
  JOURNAL
           IMMUNOL. (1993):78, 364-370
           VH domain SCANNED IN FROM JOURNAL
COMMENT
           AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES
           Residue 963 is G > T leading to silent mutation in all clones
FEATURES
  SITES
           Note
BASE COUNT
               333 a
                        439 c
                                 379 g
                                         253 t
ORIGIN
                 7
                               LEAPER -
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GIGCAGCIGG IGCAGTCIGG GGCAGAGGIG AAAAAGCCIG GGGCCTCAGI GAAGGIGICC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGITCA AGGGCCGAGT GACAGICACT AGAGAÇAÇAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTIC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC .CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACCCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      121 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
      781 ITCCTCTTCC CCCCANANCC CRAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
      841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
      901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
      961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
     1021 IGCAAGGTCT CCAACAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
     1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCCAT CCCGGGATGA GCTGACCAAG
     1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
     1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
     1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
     1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCRGAGAGC
     1381 CTCTCCCTGT CTCCGGGTAA ATGA
                                 * Anneupy Dume Fusions made Mere (34->39.)
                     lower hinge region
                                                   HEANY CHAIN.
                       Fab's Fusions were Made at this points.
           Those with HYBRIB HINGES ARE MITTERED FORTHER
       THIS PART GACAAAACTGACACA
```

AFTER THIS SEQUENCE YOUGET THE
MYBRID HINGE & LINKER SEQUENCES
Than DNAZE I (eg Fab-DNase construct pAS302)

		4-4	1	
		TIC	ધ્ય	7
		GCA GCC TTC	A	hu DNAME
		GCA	Æ	-중
		AIC	g H	
		AAG 1	, 3C	
136		Cre	2 +7	
body-DNas		GGG CTG	30	7
body		ეტე ეტე		0.3
anti		AGC	ည်	1 18 1166
ole		990	၃ ၃ ဖ	
f wb		CCG GGT AAA G	K X	
o no		GGT	30	
fusi		922	3 64	
the		ر در در	S	TWF P
in	34/37		ر د د	
lved	pAS		S	
thyc	ucts	() ()	T T	
Oligos involved in the fusion of whole antibody-DNase	Constructs pAS34/37	AS79	, , ,	
	` ,			

Constructs pAS35/38

GCA GCC TTC AAC ATC GCA GCC TTC AAC TAG I A A F N [xe hu Druhae I AAG ATC TTC TAG K I CTC CAC L AAG TTC K 666 AGC 66C 666 K AGC 66C TCG CCG S G fusion of AGA AGA S the GAG AGG GAC L S L Constructs pAS36/39 GAG AGG GAC L S L involved in Oligos AS81 AS82 AS83 AS84

Constructs pAS23/27

GGG CTG AAG ATC GCA GCC TTC AAC CCC GAC TTC TAG G L K I A A F N GAA GGG AGC GGC G CTT CCC TCG CCG C GCA CCT CGT GGA アカクラ 66T P 五五石 GGT GGC ACG AS73 AS74

Had dry strik tim had him and had title then

Harry Harry Harry and the sales

(A) pAS23

06-MAR-1995 1554 bp PRImRNA PAS23.DNA LOCUS Humanised HMFG1 Fab'2 fused to human DNase I (construct 1) DEFINITION ACCESSION NID KEYWORDS DNase I. DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) Homo sapiens ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL MEDLINE 91067672 468 c 434 g 308 t 344 a BASE COUNT ORIGIN

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//

Figure 5 (B)

```
25-AUG-2000
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                                                    SYN
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LOCUS
DEFINITION
* CCESSION
 :.YWORDS
TOURC €
                     Location/Qualifiers
~ ATURES
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     fraq
                     /note="1 to 66 of 23/27linker"
                     join(721..>735,<736..786)</pre>
     frag
                     /note="1 to 78 of 102linker [Split]"
                                            309 T
                                  435 G
                                                       0 OTHER
                          466 C
                344 A
BASE COUNT
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      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
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      841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
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Figure S (c)

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      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
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      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
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      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
      781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
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      901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
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      1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
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5′

. File: PAS23.DNA Range: 1 - 1554 Mode: Normal Codon Table: Universal FIGURE 5 (D)

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 M	 G	 W	 S	 С	 I	 I	 L	 F	 L	v	 A	 T	 A	 Т	 G	 V	 Н
TCC	CAG	63 GTG	CAG	CTG	72 GTG		TCT		GCA	GAG	90 GTG	AAA	AAG	99 CCT	GGG	GCC	108 TCA
S	Q	-	Q	L	V	Q	S	G	A	E	V	K	K	Р	G	A	S
GTG	AAG	117 GTG	TCC	TGC	126 AAG	GCT	TCT	135 GGC	TAC	ACC	144 TTC		GCC	153 TAC	TGG	ATA	162 GAG
V	К	V	S	С	K	A	S	G	Y	${f T}$	F	S	A	Y	W	I	E
TGG	GTG	171 CGC	CAG	GCT	180 CCA	GGA	AAG		CTC		198 TGG		GGA	207 GAG	ATT	TTA	216 CCT
W	v	 R	Q	 A	P	G	К	G	L	 E	W	V	G	E	I	L	P
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 G	s	 N	N	S	 R	Y	N	<u></u> Е	K	F	К	G	R	V	$^{}$	V	${f T}$
AGA	. GAC	279 : ACA		ACA	288 AAC		GCC	297 TAC		GAG	306 CTC		: AGC	315 CTG		TCT	324 GAG
 R	D	т Т	S	T	N	T	 А	Y	<u>-</u>	E	 Լ	S	S	L	R	S	Е
GAC	C ACA	333 A GC0		C TAI	342 TAC		' GCA	351 A AGA		TAC	360 GAC		r GCC	369 TGG		GCI	378 TAC
D	T	A	 V	Y	Y	 C	A	R	s	Y	D	F	A	W	F	A	Y
TGO	G GG(38° C CA		g acʻ	396 r ct(C ACA	405 A GTC		C TC	414 A GC0		C ACC	423 C AAC		CC#	432 A TCG
- -	 G	 Q	 G	T	 L	V	T	V	s	 S	 А	S	т	K	G	P	S
GT	C TT	44 C CC															486 C CTG
 V	 F	 P	 L	 A	 P	·	 S	 K	 S	 Т	S	G	G	$^{-}$ $^{\mathrm{T}}$	A	А	L
GG	C TG	49 C CT									52 G GT						540 C TCA
- <i>-</i> G		 : I	, Ţ	и К	ם ב	 Y	 F	' Р	– – – E	– – – , F	> V	. T	' V	S	 ₩	N	S
GG	SC GC		19 TG A(CC AC		8 C GT			.7 C TI				C CT		5 .G TC		594 A GGA
	3 A			r S	5 6	 G V		 Н Т	` F	 - I	-	A [7 L	, Č) S	S	

630 639 621 612 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG S S S L T V S S V L Y S L 702 693 675 684 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA N H K P S N N V T Y I C 747 756 738 729 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT K T H D VEPK S C 801 810 792 774 783 765 GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG G L K I A A F N I Q \mathbf{E} E G S G 837 846 855 864 819 828 ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC T K M S N A T L V S Y I V Q I 891 900 909 873 882 TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG I A L V Q E V R D S H T A V G m L945 954 963 927 936 AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC Q D A Ď ₽ N Γ N D L 999 1008 AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG S E P L G R N S Y K E R Y L F V Y R 1044 1053 1062 1071 1080 1035 CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC P D Q V S A V D S Y Y Y D D G C E P 1098 1107 1116 1125 1134 1089 TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG C G N D T F N R E P A I V R F F S R 1143 1152 1161 1170 1179 1188 TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC TEVREFAIVPLHAAPGD 1197 1206 1215 1224 1233 1242 GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA A V A E I D A L Y D V Y L D V Q E K 1251 1260 1269 1278 1287 1296 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT W G L E D V M L M G D F N A G C S Y 1305 1314 1323 1332 1341 1350 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG 1359 1368 1377 1386 1395 1404 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT W L I P D S A D T T A T P T H C A Y 1413 1422 1431 1440 1449 1458 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG D R I V V A G M L L R G A V V P D S 1467 1476 1485 1494 1503 1512 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA A L P F N F Q A A Y G L S D Q L A Q 1521 1530 1539 1548 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' A I S D H Y P V E V M L K *

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  AUTHORS
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Figure 6 (B)

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1561 CCCAAAAGA AGCGCAAGGT TTGA

Figure 6(c)

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                                           311 T
                                                       0 OTHER
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                                  449 G
                355 A
BASE COUNT
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Range:

1 - 1584 Mode: Normal

FIGURE 6(D) Codon Table : Universal 18 27 36 45 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC I I L F L V Γ 63 72 81 90 99 108 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA SQVQLVQSGAEVK K P G A S 117 126 135 144 153 162 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG T F V K V S C K A S G Y 171 180 189 198 207 216 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT WVRQAPGKGLEWVGEILP 234 252 225 243 261 270 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT S R Y N E K F K G NR V 279 288 297 306 315 324 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG R D T S T N T A Y M E L S S L R S E 360 333 342 351 369 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC 387 396 405 414 423 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G Q G T L V T V S S A S T K G P S 441 450 459 468 477 486 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A L 504 513 522 531 540 495 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S 549 558 567 576 585 594 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA G A L T S G V H T F P A V L Q S S G

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639 621 630 612 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S 702 684 693 675 657 666 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA H K P S N T K N V N T Y I C 756 738 747 729 711 720 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT C P A P K T H T C V E P K S C D 801 810 783 792 765 774 GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG EGSGGLKIAAFNI \mathbf{r} 837 855 864 846 828 819 ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC T K M S N A T L V S Y I V Q I 909 918 900 891 882 873 TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG D I A L V Q E V R D S H L T A V G 945 963 954 927 936 AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC K L L D N L N Q D A P D T Y H 999 1008 1017 990 981 AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG S E P L G R N S Y K E R Y L F V Y R 1035 1044 1053 1062 1071 1080 CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC P D Q V S A V D S Y Y Y D D G C E P 1098 1107 1116 1125 1134 1089 TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG C G N D T F N R E P A I V R F F S R 1143 1152 1161 1170 1179 1188 TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC F T E V R E F A I V P L H A A P G D 1197 1206 1215 1224 1233 1242 GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA A V A E I D A L Y D V Y L D V Q E K 1251 1260 1269 1278 1287 1296 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT W G L E D V M L M G D F N A G C S Y 1314 1323 1332 1341 1350 1305 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG 1368 1377 1386 1395 1404 1359 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT W L I P D S A D T T A T P T H C A Y 1422 1431 1440 1449 1458 1413 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG DRIVVAGMLLRGAVVPDS 1476 1485 1494 1503 1512 1467 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA A L P F N F Q A A Y G L S D Q L A Q 1530 1539 1548 1557 1566 1521 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA A I S D H Y P V E V M L K G G G P K 1575 1584 AAG AAG CGC AAG GTT TGA 3'

1575 1584

AAG AAG CGC AAG GTT TGA 3

K K R K V *

(A) pAS34

2196 bp 2196 bp DNA 14-AUG-1998 2196 bp LOCUS PAS34.DNA HUMANISED HMFG1 heavy chain fused to human DNAse construct 34 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) DEFINITION REFERENCE VERHOEYEN ET AL AUTHORS CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS79 and AS80 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) FEATURES Residue 963 is G > T leading to silent mutation in all clones FEATURES SITES Note 607 g 411 t 677 c BASE COUNT 501 a ? ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGCCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG 1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG 1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG 1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG 1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG 1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC 1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC 1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC 1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC 1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC 1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT 2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG 2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC 2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

11

File: PAS34.DNA'
Range: 1 - 2196 Mode: Normal FIGURE 7 (B) Codon Table : Universal 45 27 36 18 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC W S C I I L F L V A T A T G V H 99 108 81 90 72 63 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA S Q V Q L V Q S G A E V K K P G A S 153 144 135 126 117 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG K A S G Y T F S A Y V K V S C 189 198 207 180 171 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT W V R Q A P G K G L E W V G E I L P 261 270 252 243 234 225 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT G S N N S R Y N E K F K G R V T V T 324 315 306 297 288 279 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG N T A Y M E L S S L R S E R D T S T 360 369 351 342 333 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC T A V Y Y C A R S Y D F A W F A Y 405 414 423 396 387 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G Q G T L V T V S S A S T K G P 468 477 486 441 450 459 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A L 495 504 513 531 522 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S 549 558 567 576 585 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA G A L T S G V H T F P A V L Q S S G 603 612 621 630 639 648 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S L G T Q 684 693 702 657 666 675 -] -

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA Y I C N V N H K P S N J. 747 756 738 729 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT S C D K T H T C V E P K 810 801 792 783 774 765 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC E L L G G P S V F K РK L 837 846 855 828 819 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC L M I S R T P E V T C V V V D V S H 909 918 900 891 882 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT V K F N W Y V D G V E V H N 963 972 954 945 936 927 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC AKTKPREEQYNST Y R 1026 999 1008 1017 990 981 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG L T V L H Q D W L N G K E Y K C K 1062 1071 1080 1044 1053 1035 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1125 1134 1116 1107 1098 1089 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG Q P R E P Q V Y T L P P S R D E L 1143 1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y P S D 1197 1206 1215 1224 1233 1242 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T 1251 1260 1269 1278 1287 1296 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG PPVLDSDGSFFLYSKLTV 1305 1314 1323 1332 1341 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E

1377 1386 1395 1404 1359 ' 1368 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG A L H N H Y T Q K S L S P G K 1458 1422 1431 1440 1449 1413 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG G G L K I A A F N I Q T F G E 1503 1494 1476 1485 1467 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC M S N A T L V S Y I V Q I L S R Y D 1530 1539 1548 1557 1566 1521 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG I A L V Q E V R D S H L T A V G K L 1584 1593 1602 1611 1620 1575 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG D N L N Q D A P D T Y H Y V V S E 1665 1656 1647 1638 1629 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC P L G R N S Y K E R Y L F V Y R P D 1683 1692 1701 1710 1719 1728 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG Q V S A V D S Y Y Y D D G C E P C G 1755 1764 1773 1782 1746 1737 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA N D T F N R E P A I V R F F S R F T 1800 1809 1818 1827 1836 1791 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V 1845 1854 1863 1872 1881 1890 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC A E I D A L Y D V Y L D V Q E K W G 1899 1908 1917 1926 1935 1944 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA L E D V M L M G D F N A G C S Y V R 1962 1971 1980 1989 1998 1953 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG PSQWSSIRLWTSPTFQWL 2052 2025 2043 2034 2016 2007 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R

2061 2070 2079 2088 2097 2106

ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT

I V V A G M L L R G A V V P D S A L

2115 2124 2133 2142 2151 2160

CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC

P F N F Q A A Y G L S D Q L A Q A I

2169 2178 2187 2196

AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

S D H Y P V E V M L K *

FIGURE 8

(A) <u>pAS35</u>

DNA 14-AUG-1998 2193 bp 2193 bp PAS35.DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse construct 35 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G) DEFINITION REFERENCE VERHOEYEN ET AL AUTHORS CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS81 and AS82 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** In 17.12.1 residue 1398 is A > G (silent K to K mutation) FEATURES SITES Note 606 g 410 t 500 a 677 c BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGAAgGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC 1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT 1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT 2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA

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File: PAS35.DNA
Range: 1 - 2193 Mode: Normal
Codon Table: Universal

FIGURE 8(8)

																	•
ATG (GGA	9 TGG	AGC	TGT	18 ATC	ATC	CTC				-	ACA			GGT	GTC	54 CAC
 		 W	 S	 C	- - -	 I	 L	 F	 L	 V	 A	 T	 A	 Т	 G	 V	 Н
TCC (CAG	63 GTG	CAG	CTG	72 GTG	CAG	тст	81 GGG	GCA	GAG	90 GTG	AAA	AAG	99 CCT	GGG	GCC	108 TCA
S	 Q	v	Q	 L	ν	 Q	 S		 A	E	v		K	P	 G	A	 S
GTG	AAG	117 GTG	TCC									AGT		153 TAC	TGG	ATA	162 GAG
v	 К	v	- \$	C	- К	A	S	G	Y	T	F	S	A	Y	~ W	 I	E
TGG	GTG	171 CGC	CAG	GCT	180 CCA	GGA	AAG		СТС			GTC		207 GAG	ATT	TTA	216 CCT
W	v	 R	Q	A	P	G	 К	G		E	W	V	G	E	I		P
GGA	AGT	225 AAT	TAA	TCT	234 AGA	TAC	TAA	243 GAG		TTC	252 AAG	GGC	CGA	261 GTG		GTC	270 ACT
G	S	N	N	s	R	Y	N	E	K	F	K	G	R	v	T	v	T
AGA	GAC	279 ACA	TCC	ACA	288 AAC		GCC					AGC				TCT	324 GAG
R	D	Ţ	- S	T	N	 Т	A	Y	~- - М	- - Е	 L	S	S	L	- R	s	- Е
GAC	ACA	333 GCC		TAT	342 TAC							TTT		369 TGG		GCT	378 TAC
D	T	A	Λ	Y	Y	C	A	R	S	Y	D	F	A	- W	- - -	A	Y
TGG	GGC	387 CAA		ACT								TCC				CCA	432 TCG
W	G	Q	G	${f T}$	L	V	Ţ	V	S	S	Α	S	${f T}$	K	G	P	S
GTC	TTC	441 CCC			450 CCC				AGC			GGG				GCC	486 CTG
V	F	P	L	Α	P	S	S	K	S	Т	S	G	G	\mathbf{T}	A	Α	L
GGC	TGC											ACG					540 TCA
G	С	L	V	K	D	Y	F	Р	E	P	V	Т	V	S	W	N	S
GGC	GCC											GTC					594 GGA
G	A	L	T	S	G	V	H	Т	F	P	A	V	L	Q	S	S	G
СТС	: TA(603 TCC															648 CAG
I	Y	S	L	S	s	V	V	T	V	P	S	S	S	 L	G	T	Q
		651	7		666	5		679	5		684	1		690	3		702

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA Y I C N V N H K P S N \mathbf{T} 729 738 747 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT DKTHTC P P V E P K S C 801 810 783 792 774 765 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC ELLGGPSVFLFPPKDT 855 846 837 828 819 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC M I S R T P E V T C V V V D V S H 909 918 882 891 900 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT EDPEVKFNWYVDGV E 945 954 963 972 936 927 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC A K T K P R E E Q Y N S T Y R V V S 1008 1017 999 990 981 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K 1062 1071 1080 1053 1035 1044 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA SNKALPAPIEKTISKAK 1107 1116 1125 1098 1089 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1143 1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y P S D 1233 1242 1215 1224 1206 1197 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T 1251 1260 1269 1278 1287 1296 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG P P V L D S D G S F F L Y S K L T V 1305 1314 1323 1332 1341 1350 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E

1377 1386 1395 1404 1359 1368 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC A L H N H Y T Q K S L S P K G 1422 1431 1440 1449 1458 1413 GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG G L K I A A F N I Q T F G E T K M 1503 1485 1494 1467 1476 TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC S N A T L V S Y I V Q I L S R Y D I 1530 1539 1548 1557 1566 1521 GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG A L V Q E V R D S H L T A V G K L L 1575 1584 1593 1602 1611 1620 GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA D N L N Q D A P D T Y H Y V V S E P 1665 1656 1647 1638 1629 CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG L G R N S Y K E R Y L F V Y R P D Q 1692 1701 1710 1719 1683 GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC V S A V D S Y Y Y D D G C E P C G N 1746 1755 1764 1773 1782 1737 GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG D T F N R E P A I V R F F S R F T E 1800 1809 1818 1827 1836 1791 GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC V R E F A I V P L H A A P G D A V A 1854 1863 1872 1881 1890 1845 GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG E I D A L Y D V Y L D V Q E K W G L 1899 1908 1917 1926 1935 1944 GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC E D V M L M G D F N A G C S Y V R P 1953 1962 1971 1980 1989 1998 TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC S Q U S S 1 R L W T S P T F Q W L I 2025 2034 2043 2052 2007 2016 CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC PDSADTTATPTHCAYDRI

2061 2070 2079 2088 2097 2106

GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC

V V A G M L L R G A V V P D S A L P

2115 2124 2133 2142 2151 2160

TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT

F N F Q A A Y G L S D Q L A Q A I S

GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

D H Y P V E V M L K *

figure 9

(a) pAS36

2190 bp 2190 bp 14-AUG-1998 DNA PAS36.DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse - construct 36 DEFINITION Clone 18.24.1 with residue 1392 T > C DEFINITION REFERENCE VERHOEYEN ET AL **AUTHORS** CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS83 and AS84 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) FEATURES Residue 963 is G > T leading to silent mutation in all clones FEATURES Residue 1392 T > C silent S to S mutation **FEATURES** SITES Note 605 g 409 t 678 c 498 a BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CcCCGGGGAG CGGCGGCCTG AAGATCGCAG CCTTCAACAT CCAGACATTT 1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC 1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG 1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG 1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG 1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA 1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT 1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC 1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG 1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC 1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT 2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT 2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC 2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA

11

File : PAS36.DNA

FIGURE 9 (B) 2190 Mode: Normal Range: 1 -Codon Table : Universal 27 36 45 18 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC W S C I I L F L V A T A 108 99 90 81 72 63 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA E V K G A S Q V Q L Q S 153 144 135 126 117 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG Y \boldsymbol{A} S Y F G S Α K 207 216 189 198 180 171 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT W V R Q A P G K G L E W 270 252 261 243 234 225 GGA AGT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT R Y N E K F K G R V S N 324 315 306 288 297 279 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG S L R S E Y M E L S Α 378 369 360 351 342 333 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC A Y F Y D A RS C 414 423 405 396 387 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG G Q G T L V T V S S A S T K G P S 477 441 450 459 468 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A L 540 504 513 522 531 495 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S 558 567 576 585 594 549 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA G A L T S G V H T F P A V L Q S S G 648 630 612 621 639 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S L G T Q 657 666 675 684 693 702 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA Y I C N V N H K P S N T K V D K K 756 747 738 729 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT S C D K T H T C P P C P A P K 810 792 801 783 774 765 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC K P K E L L G G P S V F L F 837 846 855 828 819 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC L M I S R T P E V T C V V D V S H 918 909 900 891 882 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E V K F N W Y V D G V E V H N 972 963 954 945 936 927 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC AKTKPREEQYNSTYRVVS 1017 1008 990 999 981 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K 1053 1062 1071 1080 1044 1035 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA S N K A L P A P I E K T I S K A K 1089 1098 1107 1116 1125 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1152 1161 1170 1179 1188 1143 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- $\begin{smallmatrix}T&&K&&N&&Q&&V&&S&&L&&T&&C&&L&&V&&K&&G&&F&&Y&&P&&S&&D\end{smallmatrix}$ 1197 1206 1215 1224 1233 1242 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---I A V E W E S N G Q P E N N Y K T T 1251 1260 1269 1278 1287 1296 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG PPVLDSDGSFFLYSKLTV 1341 1332 1323 1314 1305 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG --- --- --- --- --- --- --- --- --- --- --- --- ---D K S R W Q Q G N V F S C S V M H E

1368 1377 1386 1395 1359 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC A L H N H Y T Q K S L S P 1422 1431 1440 1458 1449 1413 GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC L K I A A F N I Q T F G E T K M S 1503 1485 1494 1476 1467 AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC N A T L V S Y I V Q I L S R Y D I A 1530 1539 1548 1557 1566 1521 CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC L V Q E V R D S H L T A V G K L L D 1584 1593 1602 1611 1620 1575 AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG N L N Q D A P D T Y H Y V V S E P L 1665 1674 1656 1647 1638 1629 GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG R P D O V G R N S Y K E R Y L F V Y 1692 1701 1710 1719 1728 1683 TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC P C G N D S A V D S Y Y Y D D G C Ε 1755 1764 1773 1782 1746 1737 ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG GTC F N R E P A I V R F F S R F T E V 1791 1800 1809 1818 1827 AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG REFAIVPLHAAPGDAVAE 1854 1863 1872 1881 1890 1845 ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG I D A L Y D V Y L D V Q E K W G L E 1899 1908 1917 1926 1935 1944 GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC ___ __ __ __ __ __ __ __ __ __ __ ___ ___ ___ ___ D V M L M G D F N A G C S Y V R P S 1962 1971 1980 1989 1998 1953 CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC Q W S S I R L W T S P T F Q W L I P 2052 2034 2043 2025 2007 2016 GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG D S A D T T A T P T H C A Y D R I V

2061 2070 2079 2088 2097 2106

GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT

V A G M L L R G A V V P D S A L P F

2115 2124 2133 2142 2151 2160

AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC

N F Q A A Y G L S D Q L A Q A I S D

2169 2178 2187

CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

H Y P V E V M L K *

FIGURE 10

(A) <u>pAS37</u>

2226 bp 2196 bp 2196 bp DNA 14-AUG-1998 LOCUS PAS37.DNA HUMANISED HMFG1 heavy chain fused to human DNAse construct 37 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) plus NLS DEFINITION REFERENCE VERHOEYEN ET AL AUTHORS TITLE CONSTRUCTION OF RESHAPED HMFG1 etc IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS79 and AS80 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones FEATURES SITES Note 619 g BASE COUNT 511 a 683 c 413 t ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG 1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG 1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG 1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG 1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG 1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC 1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC 1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC 1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC 1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC 1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT 2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG 2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC 2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGGGG GACCCAAAAA GAAGCGCAAG 2221 GTTTGA

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File: PAS37.DNA
Range: 1 - 2226
Codon Table: Universal Mode : Normal

FIGURE 10 (B)

																	/
ATG (GGA	9 TGG	AGC								36 GCA				GGT	GTC	54 CAC
	 G	 W	S		 I	 I	 	 F	 L	 V	 А	 Т	 А	T	G	V	 Н
TCC (CAG	63 GTG	CAG	CTG		CAG						AAA	AAG	99 CCT	GGG		108 TCA
	Q	 V	Q	 L	V	Q	 S	 G	Α	E	V		K	P	G	 А	s
GTG		117 GTG	TCC								144 TTC						162 GAG
v	 K	V	S	C	K	 А	S	G	Y	T	F	S	A	Y	W	I	E
TGG	GTG	171 CGC	CAG	GCT	180 CCA					GAG	198 TGG	GTC	GGA	207 GAG	АТТ	TTA	216 CCT
W	V	R	Q	Α	P	G	K	G	L	E	W	V	G	E	I	L	P
GGA	AGT	225 AAT	ТАА	TCT	234 AGA	TAC	AAT	243 GAG	AAG	TTC	252 AAG			261 GTG	ACA	GTC	270 ACT
G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	${f T}$	V	T
AGA	GAC	279 ACA		ACA							306 CTC				AGG	TCT	324 GAG
R	D	$^{}$	S	Т	N	T	A	Y	M	E	L	S	S	L	R	S	E
GAC	ACA	333 GCC				TGT					360 GAC		GCC			GCT	378 TAC
D	Т	A	V	Y	Y	С	A	R	S	Y	D	F	A	W	F	A	Y
TGG	GGC	387 CAA									414 GCC					CCA	432 TCG
W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	₽	S
GTC	TTC	441 CCC									468 TCT						486 CTG
V	F	P	L	А	P	S	S	K	S	T	S	G	G	${f T}$	A	A	L
GGC	TGC	495 C CTC)AA :	504 GAC					A CCC			GT0			AAC	540 TCA
G	С	L	V	K	D	Y	F	P	E	P	V	${f T}$	V	S	W	N	S
GGC	GCC	549 CTC		C AGG		3 C GT(CT <i>I</i>			C TCA	594 A GGA
G	А	L	T	S	G	V	Н	${ m T}$	F	P	А	V	L	Q	S	S	G
CTC	C TA	60 C TC		C AG	61: C AG0						630 C TC0					C AC(648 C CAG
L	Y	S	L	S	S	V	V	т	V	Р	S	S	S	L	G	Т	Q
		65	7		66	6		67	5		684	1		69	3		702

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA N H K S N 729 720 738 747 756 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H T 765 774 783 792 801 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC F K P K 819 828 837 846 855 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC I S R ${f T}$ P E V ${f T}$ 873 882 891 900 909 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E D P E V K F N W Y V D G V 927 936 945 954 963 972 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC AKTKPRE E Q Y N S Y R ${f T}$ 990 999 1008 1017 981 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG Η Q D W ${f L}$ N G K 1035 1044 1053 1062 1071 1080 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA S N K A L Α ₽ I E K 1089 1098 1107 1116 1125 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1143 1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N O V S L T C L V K G F Y P S D 1197 1206 1215 1224 1233 1242 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T 1251 1260 1269 1278 1287 1296 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG P P V L D S D G S F F L Y S K L T V 1305 1314 1323 1332 1341 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG <u>---</u> D K S R W Q Q G N V F S C S V M H E

1377 1386 1395 1404 1368 1359 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG Q K S L S L S P G K G ALHNHYT 1422 1431 1440 1449 1413 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG G G L K I A A F N I Q T F G E T K 1476 1485 1494 1503 1512 1467 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC MSNATLVSYIVQILSRYD 1539 1548 1557 1566 1530 1521 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG I A L V Q E V R D S H L T A V G K L 1611 1593 1602 1584 1575 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG L D N L N Q D A P D T Y H Y V V S E 1638 1647 1656 1665 1674 1629 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC P L G R N S Y K E R Y L F V Y R P D 1701 1710 1719 1692 1683 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG Q V S A V D S Y Y Y D D G C E P C G 1764 1773 1782 1755 1746 1737 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA D T F N R E P A I V R F F S R F T 1809 1818 1800 1791 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V 1863 1872 1881 1890 1854 1845 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC A E I D A L Y D V Y L D V Q E K W G 1935 1944 1926 1917 1908 1899 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA L E D V M L M G D F N A G C S Y V R 1953 1962 1971 1980 1989 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG PSQWSSIRLWTSPTFQWL 2007 2016 2025 2034 2043 2052 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R

2061 2070 2079 2088 2097 2106

ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT

I V V A G M L L R G A V V P D S A L

2115 2124 2133 2142 2151 2160

CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC

P F N F Q A A Y G L S D Q L A Q A I

AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG

S D H Y P V E V M L K G G G P K K K

2223
CGC AAG GTT TGA 3'

(A) pAS38

14-AUG-1998 2193 bp DNA 2223 bp PAS38.DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse construct 38 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS DEFINITION REFERENCE VERHOEYEN ET AL AUTHORS CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS81 and AS82 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) FEATURES Residue 963 is G > T leading to silent mutation in all clones FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation) FEATURES SITES Note 618 g 510 a 412 t 683 c BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGACA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGAAgGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC 1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT 1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT 2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGGGGGGCGCC CCAAAAAGAA GCGCAAGGTT 2221 <u>TGA</u>

LOMES

File: PAS38.DNA

Range: 1 - 2223 Mode: Normal FIGURE 11 (B) Codon Table : Universal 45 36 27 9 18 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC C I I L F L V A T A T G V H 99 108 90 72 81 63 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA S G A E V K V Q 153 162 144 135 126 117 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG K A S G Y ${f T}$ 207 198 189 171 180 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT \mathbf{P} \mathbf{G} K G L E WVRQA 270 261 252 234 243 225 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT S R Y N E K F K G R 324 315 297 306 288 279 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG A Y M E L S S N T ${f T}$ R D T 369 378 351 360 333 342 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC Α Α R S Y D Α 423 432 414 405 396 387 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G Q G T L V T V S S A S T K G P S 459 468 477 486 441 450 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A L 522 531 513 495 504 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S 549 558 567 576 585 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA G A L T S G V H T F P A V L Q S S G 603 612 621 630 639 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S L G T Q 657 666 675 684 693 702 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V NΗ K P N T K V D K K 711 720 729 738 747 756 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H 765 774 783 792 801 810 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC ELLGGPSVFLFPPKDT 819 828 837 846 855 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC MISRTP E V ${f T}$ 873 882 891 900 909 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E D P E V K F N W Y V D G 927 945 954 963 972 936 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC AKTKPREEQYNSTYRVVS 981 990 1008 1026 999 1017 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K 1035 1044 1053 1062 1071 1080 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1089 1098 1107 1116 1125 1134 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1143 1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y P S D 1197 1206 1215 1224 1233 1242 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T 1251 1260 1269 1278 1287 1296 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---P P V L D S D G S F F L Y S K L T V 1305 1314 1323 1332 1341 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---D K S R W Q Q G N V F S C S V M H E

1368 1377 1386 1395 1404 1359 , GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC A L H N H Y T Q K S L S P 1440 1449 1458 1431 1422 1413 GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG <u>G G L K I A A F N I Q T F G</u> **1476 1485 1494** 1503 1467 TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC N A T L V S Y I V Q I L S R Y D I 1539 1548 1557 1566 1530 1521 GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG A L V Q E V R D S H L T A V G K L L 1593 1602 1611 1575 1584 GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA D N L N Q D A P D T Y H Y V 1665 1638 1647 1656 1629 CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG L G R N S Y K E R Y L F V Y R P D Q 1701 1710 1719 1728 1683 1692 GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC V S A V D S Y Y Y D D G C E P C G N 1746 1755 1764 1773 1782 1737 GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG REPAIVRFFSR N 1800 1809 1818 1827 1836 GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC V R E F A I V P L H A A P G D A V A 1845 1854 1863 1872 1881 1890 GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG ___ __ __ __ __ ___ ___ ___ ___ ___ ___ EIDALYDVYLDVQEKWGL 1917 1926 1935 1944 1899 1908 GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC E D V M L M G D F N A G C S Y V R P 1980 1962 1971 1989 1953 TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC SQWSSIRLWTSPT F Q W L I 2007 2016 2025 2034 2043 2052 CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC P D S A D T T A T P T H C A Y D R I

2061 2070 2079 2088 2097 2106

GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC

V V A G M L L R G A V V P D D S A L P

2115 2124 2133 2142 2151 2160

TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT

F N F Q A A Y G L S D Q L A Q A I S

GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC

D H Y P V E V M L K G G G G P K K K R

2223
AAG GTT TGA 3'
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FIGURE 12

(4) pAS39

14-AUG-1998 2220 bp 2190 bp DNA PAS39.DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse - construct 39 DEFINITION Clone 18.24.1 with residue 1392 T > C + NLS DEFINITION REFERENCE VERHOEYEN ET AL AUTHORS CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS83 and AS84 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) FEATURES Residue 963 is G > T leading to silent mutation in all clones FEATURES Residue 1392 T > C silent S to S mutation **FEATURES** SITES Note 617 g 411 t 684 c 508 a BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CcCCGGGGAG CGGCGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT 1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC 1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG 1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG 1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG 1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA 1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT 1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC 1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG 1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC 1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT 2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT 2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC 2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

11

File: PAS39.DNA
Range: 1 - 2220
Codon Table: Universal Mode : Normal

5 '

FIGURE 12(B)

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rcc	CAG	GI	rG	CAG	CTG	GTG	CAG	TCT	GGG	G GC	A GA 	.G G'	TG 	AAA 	AAG	CC,	T GG 	GG(GCC 	TCA 	5
S	Q	,]	Q	L	V	Q	S	G									3			_
GTG	AA	10 G G1	17 IG	TCC	TGC	126 A AG	GC1	r TCI	13 r GG	5 C TA	C AC	1 CC T	44 TC	AGT	GCC	15 TA	3 .C T	GG .	ATA	162 GAG	
								 S			. – – -						_	•			
TGG	GT	1 G C	71 GC	CAG	GC1	180 CC2) A GG:	A AA	18 G G G	9 IC C 1	rc g	1 AG T	.98 rgg	GTC	: GG2	20 A G <i>P</i>)7 AG A		TTA	21 CC	
 W	 V		 R	 Q															L	P	
GGF	A AC	2 3T <i>1</i>	225 AAT	' AA	r TC'	23. T AG.	4 A TA	C AA	24 T G	43 AG A	AG I	TC I	252 AAG	GG(c cg	20 A G'	61 TG <i>P</i>	ACA	GTC	27 AC	
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AG	A G	ac 2	279 AC <i>I</i>) A TC	c ac	28 A AA	8 .c ac	CA GO	CC T	AC A	TG (GAG	CTC	AG	C AG	SC C	15 TG /	AGG	TCT	32 c G2	24 AG
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GA	.C A	.CA	33: GC(3 C G1	rc TA	34 AT T <i>A</i>	12 AC T	GT G	3 CA <i>P</i>	51 \GA '	rcc	TAC	364 GA	0 C TI	T G	3 CC 1	369 rgg	TTT	GC'		78 AC
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G'	TC '	TTC	44 C0	rc c	TG G	CA C	CC 1	rcc f	rcc	AAG	AGC	ACC	T(CT G	GG (GC	ACA	GC	G G(CC (486 CTG
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G	GC	TGC	4 : C	95 TG (GTC A	? AAG (504 GAC	TAC	TTC	513 CCC	GAA	CCC	5 G G	22 TG <i>l</i>	ACG (GTG	531 TCG		SG A		540 TC
_	. – – G	 C						 Y							T	V	S			N	S
,	200	000	5	349 STC	NCC	ልርር	558 GGC	GTG	CAC	567 ACC	TTC	c cc	5 G G	76 CT (GTC	СТА	585 CAC	5 3 T(CC I	'CA	59 GG
				.1G . L	дес Т	 S		 V			·						 Q		 S	 S	
	G			- - 0 3			612			621	L		(530			63	9			64
	CTC	TA	.C '	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GT(G CC	CC 1	rcc 	AGC	AGC	TT)	G G 			
	ľ	Y	,	S	L	S	S	V	V	Т	V	I	?	S	S	S	L		G	T	(
				657			666			67	5			684			69	3			7(

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 747 756 729 738 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT E P K S C D K T H T 774 783 792 801 810 765 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC ELLGGPSVFLFPPKDT 855 837 846 828 819 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC LMISRTPEVTCVVVDVSH 891 900 909 918 882 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT V K F N W Y V D G V 963 945 954 927 936 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC A K T K P R E E Q Y N S T Y 999 1008 1017 1026 990 981 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K 1044 1053 1062 1071 1080 1035 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA SNKALPAPIEKTISKAK 1098 1107 1116 1125 1134 1089 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1143 1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y P S D 1197 1206 1215 1224 1233 1242 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T 1269 1278 1287 1296 1260 1251 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG PPVLDSDGSFFLYSKLTV 1305 1314 1323 1332 1341 1350 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E

1359 1377 1395 1368 1386 1404 ·GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC A L H N H Y T Q K S L S L 1422 1431 1440 1449 1458 1413 GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC G L K I A A F N I Q T F G E T K M S 1476 1485 1494 1503 1467 1512 AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC NATL V S Y I V Q I L S R Y D I A 1539 1548 1521 1530 1557 1566 CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC L V Q E V R D S H L T A V G K L L D 1584 1593 1602 1611 1575 AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG N L N Q D A P D T Y H Y V V S E P L 1629 1638 1647 1656 1665 GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG GRNSYKERYLFVYRPDOV 1683 1692 1701 1710 1719 1728 TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC S A V D S Y Y Y D D G C 1737 1746 1755 1764 1773 1782 ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC FNREPAIVRFFS 1791 1800 1809 1818 1827 AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG R E F A I V P L H A A P G D A V A E 1845 1854 1863 1872 1881 ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG I D A L Y D V Y L D V Q E K W G L E 1899 1908 1917 1926 1935 1944 GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC D V M L M G D F N A G C S Y V R P S 1953 1962 1971 1980 1989 1998 CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC Q W S S I R L W T S P T F O W L I P 2007 2016 2025 2034 2043 2052 GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG D S A D T T A T P T H C A Y D R I V

2061 2070 2079 2088 2097 2106

GTT GCA GGG ATG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT

V A G M L L R G A V V P D S A L P F

2115 2124 2133 2142 2151 2160

AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC

N F Q A A Y G L S D Q L A Q A I S D

2169 2178 2187 2196 2205 2214

CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC AAG

H Y P V E V M L K G G G G G P K K K R K

GTT TGA 3'

<u>v</u> *

HYME 13

(A) pAS101

06-MAR-1995 1548 bp PRI mRNA PAS101.DNA LOCUS Humanised HMFG1 Fab'2 fused to human DNase I (pAS101) DEFINITION ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL 91067672 MEDLINE 430 g 308 t 467 c 343 a BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT 1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

11

11

. Figure 13 (B)

```
25-AUG-2000
                        1548 BP SS-DNA
                                                    SYN
           FDDNASE101
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
                     join(1..>720,<781..1548)
     frag
                     /note="1 to 1548 of PAS101.dna [Split]"
                     721..780
     fraq
                     /note="1 to 60 of 101/105linker"
                     join(721..>735,<736..>759,<760..>780)
     frag
                     /note="1 to 80 of 102linker [Split]"
                                           309 T
                                                       0 OTHER
                                  431 G
                         465 C
BASE COUNT
                343 A
RIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
327
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
      781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
      841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
      901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
      961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
     1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
     1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
     1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
     1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
     1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
     1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
      1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
     1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
     1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA
```

11

Figure 13c

```
29-AUG-2000
                         1557 BP SS-DNA
                                                    SYN
            FDDNASE101
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
                     10..1557
     fraq
                     /note="1 to 1548 of FdDNase101correct"
                     join(10..>729,<790..1557)
     frag
                     /note="1 to 1548 of PAS101.dna [Split]"
                     730..789
     frag
                     /note="1 to 60 of 101/105linker"
                     join(730..>744,<745..>768,<769..>789)
     frag
                     /note="1 to 80 of 102linker [Split]"
                                            309 T
                                  433 G
                344 A
                                                       0 OTHER
                         471 C
BASE COUNT
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
      781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
      841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
      901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
      961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
     1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
     1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
     1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCGGGGGA CGCAGTAGCC
      1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
      1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
      1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
      1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
      1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
      1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGTGA
```

* File: PAS101.DNA
Range: 1 - 1548 Mode: Normal
Codon Table: Universal

** File: PAS101.DNA
Range: 1 - 1548 Mode: Normal
** File: PAS101.DNA
Range: 1 - 1548 Mode: Normal

45 36 27 18 9 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC F L V A I ${
m L}$ Ι M G 90 99 108 81 72 63 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA G A E V K K S Q Q V Q L V 153 144 135 126 117 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG K A S G Y ${f T}$ S C 216 207 198 189 180 171 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT K G L E W Q A P G V R 270 261 252 243 234 225 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT R Y N E K F K G R V N S N 306 315 297 288 279 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG y m e L S S Α ${f T}$ T N R D T 351 360 369 378 342 333 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC D T A V Y Y C A R S Y D F A W F A Y 387 396 405 414 423 432 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G Q G T L V T V S S A S T K G P S 477 486 450 459 468 441 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A L 540 531 495 504 513 522 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S 585 594 567 576 549 558 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA GALTSGVHTFPAVLQSSG

621 630 639 648 603 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG S V L G L Y S L S S 693 675 684 702 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA P S N T Y I C N V N H K 738 747 756 720 729 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT D K T \mathbf{H} C V E P K 774 783 792 801 810 765 GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG EGGLKIAAFNIQT G K 846 855 837 864 819 828 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC S Y I V Q I L S N A T L V Μ 891 900 909 873 882 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG I A L V Q E V R D S H L T A V G K L 936 945 954 963 972 927 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG A P D ${
m T}$ Y Q D 999 1008 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC P L G R N S Y K E R Y L F V Y R P D 1044 1053 1062 1071 1080 1035 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG O V S A V D S Y Y Y D D G C E P C G 1089 1098 1107 1116 1125 1134 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ N D T F N R E P A I V R F F S R F T 1143 1152 1161 1170 1179 1188 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V 1197 1206 1215 1224 1233 1242 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC A E I D A L Y D V Y L D V Q E K W G 1251 1260 1269 1278 1287 1296 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA L E D V M L M G D F N A G C S Y V R 1305 1314 1323 1332 1341 1350 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG PSQWSSIRLWTSPTFQWL 1368 1377 1386 1395 1404 1359 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R 1413 1422 1431 1440 1449 1458 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT I V V A G M L L R G A V V P D S A L 1467 1476 1485 1494 1503 1512 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC PFNFQAAAYGLSDQLAQAI 1521 1530 1539 1548 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' S D H Y P V E V M L K *

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FIGURE 14 (A) PAS102

PRI 06-MAR-1995 1566 bp mRNA PAS102.DNA LOCUS Humanised HMFG1 Fab'2 fused to human DNase I (pAS102) DEFINITION ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1. dna) (see Figure 2) Homo sapiens ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL 91067672 MEDLINE 312 t 440 g 469 c BASE COUNT 345 a ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC 1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG 1561 AAGTGA

//

Figure 14 (B)

CUS FDI	ONASE102 1566	BP SS-DNA	SY	N 23-	MAR-2001
ABFINITION -					
ACCESSION -					
KEYWORDS -					
SOURCE -				0.000000	
BASE COUNT	345 A 468 C	440 G	313 T	0 OTHER	
ORIGIN -					00707000
1 ATGG	GATGGA GCTGTATCA	T CCTCTTCTTG	•	CTACAGGTGT	
61 GTGC	AGCTGG TGCAGTCTG	G GGCAGAGGTG	AAAAAGCCTG	GGGCCTCAGT	GAAGGTGTCC
121 TGCA	AGGCTT CTGGCTACA	C CTTCAGTGCC	TACTGGATAG	.1910001400	CCAGGCTCCA
181 GGAA	AGGGCC TCGAGTGGG	T CGGAGAGATT	TTACCTGGAA	GTAATAATTC	TAGATACAAT
241 GAGA	AGTTCA AGGGCCGAG	T GACAGTCACT	AGAGACACAT	CCACAAACAC	
301 GAGC	TCAGCA GCCTGAGGT	C TGAGGACACA	GCCGTCTATT	ACTGTGCAAG	
361 TTTG	CCTGGT TTGCTTACT	G GGGCCAAGGG	ACTCTGGTCA	CAGTCTCCTC	
421 AAGG	GCCCAT CGGTCTTCC	C CCTGGCACCC	TCCTCCAAGA	GCACCTCTGG	GGGCACAGCG
481 GCCC	TGGGCT GCCTGGTCA	A GGACTACTTC	CCCGAACCGG	TGACGGTGTC	GTGGAACTCA
541 GGCG	CCCTGA CCAGCGGCG	T GCACACCTTC	CCGGCTGTCC	TACAGTCCTC	AGGACTCTAC
601 TCCC	TCAGCA GCGTGGTGA	C CGTGCCCTCC	AGCAGCTTGG	GCACCCAGAC	CTACATCTGC
661 AACG	TGAATC ACAAGCCCA	G CAACACCAAG	GTGGACAAGA	AAGTTGAGCC	CAAATCTTGT
10 721 GACA	AAACTC ACACATGCT	G TGTCGAGTGT	CCACCGTGTC	CAGCACCAGA	GGGGAGCGGC
	TGAAGA TCGCAGCCT	T CAACATCCAG	ACATTTGGGG	AGACCAAGAT	GTCCAATGCC
841 ACCC	TCGTCA GCTACATTO	T GCAGATCCTG	AGCCGCTACG	ACATCGCCCT	GGTCCAGGAG
901 GTCA	GAGACA GCCACCTGA	AC TGCCGTGGGG	AAGCTGCTGG	ACAACCTCAA	TCAGGACGCA
961 CCAG	ACACCT ATCACTACO	T GGTCAGTGAG	CCACTGGGAC	GGAACAGCTA	TAAGGAGCGC
1021 TACC	TGTTCG TGTACAGG	CC TGACCAGGTG	TCTGCGGTGG	ACAGCTACTA	CTACGATGAT
1081 GGCT	GCGAGC CCTGCGGG	AA CGACACCTTC	AACCGAGAGC	CAGCCATTGT	CAGGTTCTTC
	GGTTCA CAGAGGTCA				
1201 GCAG	TAGCCG AGATCGAC	GC TCTCTATGAC	GTCTACCTGG	ATGTCCAAGA	GAAATGGGGC
1261 TTGG	AGGACG TCATGTTG	AT GGGCGACTTC	AATGCGGGCT	GCAGCTATGT	GAGACCCTCC
	GGTCAT CCATCCGC				
	ACACCA CAGCTACA				
	CTCCGAG GGGCCGTT		GCTCTTCCCT	TTAACTTCCA	GGCTGCCTAT
	TGAGTG ACCAACTG				
1561 AAGT					

1561 GTGATGCTGA AGTGA

Figure 14 (c)

```
29-AUG-2000
                                                    SYN
                       1575 BP SS-DNA
            FDDNASE302
LOCUS
DEFINITION
                                  pAS302
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
                     10..1575
     frag
                     /note="1 to 1566 of FdDNase102correct"
                                           313 T
                                                      0 OTHER
                         474 C
                                  442 G
BASE COUNT
                346 A
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
1/
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
      841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
      901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
      961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
     1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
     1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
     1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC
     1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
     1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
     1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
     1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
     1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
     1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
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Mode : Normal

' File : PAS102.DNA Range : 1 - 1566 Codon Table : Universal

FIGURE 14 (D)

												`	(4-	110	17	02	•
ATG	GGA	9 TGG	AGC	TGT	18 ATC	ATC	CTC	27 TTC		GTA	36 GCA	ACA	GCT	45 ACA	GGT	GTC	54 CAC
 М	 G	W	 S	- - -	 I		 L	 F	 L	 V		 Т	 A	T		 V	 H
TCC	CAG	63 GTG	CAG	СТG	72 GTG	CAG	тст	81 GGG		GAG	90 GTG	AAA	AAG	99 CCT	GGG	GCC	108 TCA
 S	 Q	 V		 L	 V	 Q	 S	 G	 A	 E	 V	 K	 K	 P	 G		S
	~	117			126			135			144			153			162
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
V	K	V	S	С	K	A	S	G	Y	Т	F	S	A	Y	W	I	E
TGG	GTG	171 CGC		GCT	180 CCA	GGA	AAG	189 GGC		GAG	198 TGG		GGA	207 GAG		TTA	216 CCT
W	v	 R	Q	A	P	G	 K	G	L	E	W	v	G	E	I	L	P
GGA	AGT	225 `AAT		TCT	234 ' AGA		TAA	243 GAG		TTC	252 AAG		C CGA	261 GTG		GTC	270 ACT
G	S		N	s	 R	Y	N	E	K	- F	 К	G	R	Λ	T	V	T
		279			288				,								324
AGA	GAC	ACA	A TC(C ACA	. AAC	: ACA		TAC	ATG	GAC	G CTC	AG(. AGC		- AGG		GAG
R	D	Т	S	Υ	N	Υ	A	Y	М	£	L	S	S	L	R	S	E
GAC	: AC	331 A GC0		С ТАП	342 TAC		r GCA		L A TCC) C TT: 		369 TGC		GC1	378 TAC
D	${ m T}$	А	V	Y	Y	С	A	R	S	Y	D	F	Α	W	F	A	Y
TGO	G GG(38° C CA			396 CTC				5 C TC(C ACC			C CCA	432 A TCG
 W	 G	 Q	 G	·	 L	· V	T	·	 S	 S	 A	 S	 T	 K	 G	P	s
GT(n TT	44 C CC		'G GC.	45) A CC			45° C AA		c ac		8 T GG			7 A GC	g gca	486 C CTG
V																	_
		49	15		50	4		51	3		52	2		53	1		540
GG	C TG	C CI	rg gr	C AA	G GA 	C TA 	C TT	C CC	C GA	A CC 	G GT	'G AC	G GT	G TC	G TG 	G AA(C TCA
G	C		. <i>\</i>	/ K	D	Y	F	. P	E	F	> V	T T	٧ ٠	' S	W	N	S
GG	C GC	54 CC C1		CC AG	55 SC GG		rg CA		57 CC TT			6 T G1		58 A CA		С ТС 	594 A GGA
G			، ۔۔۔۔۔	r s	- - -	;	7 F	 I I	r F	, <u>I</u>	? <i>1</i>	4 1	/ I.	· Č) S	S	G

612 621 630 639 648 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG S S s v \mathbf{T} V L Y S L S 675 684 693 702 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA N V N H K P S N TK V T Y I C 729 738 747 756 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG V E P K S C D K T H T C C 792 801 810 774 783 765 TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG C P A P E G S G G L K I A A F N I Q 855 837 846 828 819 ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG T K M S N A T L V S Y I V Q 891 909 900 918 873 882 ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG R D S I L S R Y D I A L V Q E V 945 954 963 972 936 927 ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT K L L D N L N Q D A P D V G 1008 1017 999 990 981 CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG H Y V V S E P L G R N S Y K E 1044 1053 1062 1071 1080 1035 TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT F V Y R P D Q V S A V D S Y Y D D 1098 1107 1116 1125 1134 1089 GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG G C E P C G N D T F N R E P A I V R 1161 1170 1179 1188 1152 1143 TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG F F S R F T E V R E F A I V P L H A 1197 1206 1215 1224 1233 1242 GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT A P G D A V A E I D A L Y D V Y L D 1251 1260 1269 1278 1287 1296 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG V Q E K W G L E D V M L M G D F N A 1305 1314 1323 1332 1341 1350 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC G C S Y V R P S Q W S S I R L W T S 1359 1368 1377 1386 1395 1404 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG PTFOWLIPDSADTTAT 1413 1422 1431 1440 1449 1458 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT H C A Y D R I V V A G M L L R G A V 1467 1476 1485 1494 1503 1512 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC V P D S A L P F N F Q A A Y G L S D 1521 1530 1539 1548 1557 1566 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' LAQAISDHYPVEVMLK*

FIGURE 15

(A) pAS103

06-MAR-1995 PRI 1560 bp mRNA PAS103.DNA LOCUS Humanised HMFG1 Fab'2 fused to human DNase I (pAS103) DEFINITION ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL MEDLINE 91067672 436 g 312 t 468 c 344 a BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC 1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

Figure 15 (B)

```
25-AUG-2000
                                                     SYN
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FINITION
# UCESSION
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SOURCE
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                     721..792
     frag
                     /note="1 to 72 of 103/107linker"
                     join(721..>771,<772..792)
     frag
                     /note="1 to 78 of 102linker [Split]"
                                   436 G
                                            313 T
                                                        0 OTHER
                         467 C
BASE COUNT
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
\mathcal{I}_{\mathcal{A}}(\mathbb{T}_{+})
      481 GCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
       961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
      1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
      1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
      1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
      1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

1561 CTGAAGTGA

Figure 15 (C)

```
29-AUG-2000
                                                    SYN
            FDDNASE103
                        1569 BP SS-DNA
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
                     /note="1 to 1560 of FdDNase103correct"
                     join(10..>729,<802..1569)
     fraq
                     /note="1 to 1560 of PAS103.dna [Split]"
                     730..801
     frag
                     /note="1 to 72 of 103/107linker"
                     join(730..>780,<781..801)
     frag
                     /note="1 to 78 of 102linker [Split]"
                                           313 T
                                  438 G
                                                       0 OTHER
                         473 C
BASE COUNT
                345 A
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGCCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
     481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT
      841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
      901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
      961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
     1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
     1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
     1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
     1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
     1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
     1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
     1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
     1441 ATGCTGCTCC GAGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
     1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
```

• File: PAS103.DNA
Range: 1 - 1560 Mode: Normal
Codon Table: Universal

5′

FIGURE 15(D)

		9							27							45				54
ATG	GGA	TGG	AG	SC 1	GT A	ATC	ATC	CTC	TTC	TTG	GTA	A G 		ACA	GCT	ACA	GGT	Г G 	TC (CAC
M	G	W	Ş	5	С	I	I	L	F	L	V		А	T	A	T	G		V	Н
rcc	CAG	63 GT0		AG (81 GGG									G G		108 TCA
																<u></u>				
S	Q	V	(Q	L	V	Q	S	G	A	Ε		V	K	K	Þ	G		A	S
GTG	AAG	11′ GT(CC '		126 AAG	GCT	тст	135 GGC				144 TTC		GCC	153 TAC		G Æ		162 GAG
v		v	_ _	 S		- - -	 A	 S	 G	Y	 T	·	 F	 S	A	Y	 W		I	 E
TGG	GTG	17 CG		AG ·	GCT	180 CCA	GGA	AAG	189 GGC						GGA		, F AT			216 CCT
 W	 v	 R		 Q	 A	 Р	 G		 G	 L	 E	- 	 W	v	G	E	 I	· ·		P
GGA	AGT	22 AA		ТA	TCT	234 AGA		raa :	243 GAG		3 T7		252 AAG	GGC	CGI	261 A G T(:A	GTC	270 ACT
- G	-			N	S	- R	 Y	N	E	K	 I	- - ?	К	G	R	V	r	3	V	T
		27				288			297				306			31				324
AGA	GA(AC	:A 1	rcc	ACA	AAC	ACA		TAC	TA:	G G/ 	AG 	CTC	AGC	: AG0	CTC	G AC 	3G 	TCT 	GAG
R	D	7		S	T	N	Т	A	Y	M	1	E	L	S	S	L	I	ર	S	Е
GAC	C AC.	33 A G0		GTC	TAT	342 TAC		r gca	351 A AG <i>I</i>		С Т.	AC	360 GAC		r GC	36 C TG		ΓT	GCT	378 TAC
 D	 T		<i>Ā</i>	 V	 Y	Y	 C	A	 R	 S	<u> </u>	 Y	D	 F	 A	– –– W		 F	 A	 У
TG	G GG		87 AA	GGG	ACT	396 CTC		C AC	40! A GT		СТ	'CA	414 GCC		C AC	42 C AA		GC	CCA	432 . TCG
	 G	 ;	 Q	 G	T	L	 V	 T		 S	 3	S	A	. <u>-</u> -	r	. K	. – –	 G	P	 S
GT	C TI		41 CC																	486 CTG
 V	 F		 P	 L	A	 P	 S	 S	 S K		5	 Т	S	 G		;	r 	A	A	L
GG	C T(95 TG	GTC	AA C			C TI		.3 :C G2					G G		31 CG T		AA	540 C TCA
G	; (C	L	V	 K	– –– D)	 ' F	F F	> ;	<i>-</i> E	P	V	T	' '	J :	S	W	N	S
GG	SC G		549 CTG	ACC	C AG	55 C GG			56 AC AC						C C				TC.	594 A GG <i>I</i>
	 3	Λ .	L	J,	 S				 H :	r 	 F		 A		7	 	Q	 S	S	 G

630 639 648 603 612 621 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 666 675 684 693 702 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA P N T Y I C N H K 729 738 747 711 720 756 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG E P K S C D K T H T C C 783 792 801 810 765 774 TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT EGGLKIAAFNIQ 819 828 837 84*6* 855 GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG T K M S N A T L V S Y Ι 891 900 909 873 882 AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC I A L 0 \mathbf{E} R D S H L 927 936 945 954 963 972 GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC G K L L D N L N Q D A Ρ T Y H Y 1008 981 990 999 1017 GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG V V S E P L G R N S Y K E R Y L F V 1035 1044 1053 1062 1071 1080 TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC Y R P D Q V S A V D S Y Y Y D D G C 1089 1098 1107 1116 1125 1134 GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC E P C G N D T F N R E P A I V R F F 1161 1170 1179 1143 1152 1188 TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG S R F T E V R E F A I V P L H A A P 1197 1206 1215 1224 1233 1242 GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA G D A V A E I D A L Y D V Y L D V Q 1251 1260 1269 1278 1287 1296 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC E K W G L E D V M L M G D F N A G C 1305 1314 1323 1332 1341 1350 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC S Y V R P S Q W S S I R L W T S P T 1359 1368 1377 1386 1395 1404 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT F Q W L I P D S A D T T A T P T H C 1413 1422 1431 1440 1449 1458 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC A Y D R I V V A G M L L R G A V V P 1467 1476 1485 1494 1503 1512 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG D S A L P F N F Q A A Y G L S D Q L 1521 1530 1539 1548 1557 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' A Q A I S D H Y P V E V M L K *

FIGURE 16

(f) pAS104

mRNAPRI 06-MAR-1995 1560 bp PAS104.DNA LOCUS Humanised HMFG1 Fab'2 fused to human DNase I (pAS104) DEFINITION Position 924 G to A by ggg to gag Linker GR instead of GG (position 777) ACCESSION NID KEYWORDS DNase I. DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) Homo sapiens ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL 91067672 MEDLINE 312 t 434 g 468 c BASE COUNT 346 a ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA 901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC 1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

11

11

Figure 16 (B)

```
25-AUG-2000
                                                     SYN
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                       1560 BP SS-DNA
CUS
DEFINITION
"CCESSION
HEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     fraq
                     /note="1 to 1560 of PAS104.dna [Split]"
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     frag
                     /note="1 to 72 of 104linker"
                     join(721..>774,<776..792)
     frag
                     /note="1 to 72 of 103linker [Split]"
                     join(721..>771,<772..>774,<776..792)
     frag
                     /note="1 to 78 of 102linker [Split]"
                                   434 G
                                            313 T
                                                       0 OTHER
                          467 C
BASE COUNT
                346 A
ORIGIN
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
1 1
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
\{\pm 3\}
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
\{A_i\}_{i=1}^n
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCAGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

File: PAS104.DNA Range: 1 - 1560 Mode: Normal Floure 16 (C) Codon Table : Universal 54 45 36 18 27 ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC F L Α I L99 108 90 81 72 63 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA V K \mathbf{E} S G A 135 144 153 126 117 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG C K A S G Y T Y F S A 207 216 198 189 180 171 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT WVRQAPGKGLE ${f E}$ W V G 243 252 261 270 234 225 GGA AGT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT S R Y N E K F K G R V 288 297 306 324 315 279 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG S T N T A Y M E L S S L R S 369 378 360 351 342 333 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC D T A V Y Y C A R S Y D F A W F 387 396 405 414 423 432 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G Q G T L V T V S S A S T K G P S 459 468 477 486 441 450 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A L 504 513 522 531 540 495 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S

549 558 567 576 585

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

648 639 630 621 612 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG S S Р L Y S L S 693 702 684 675 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA N K N H K 756 747 738 729 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG V E C C K T Н T C D С P K 783 801 792 810 774 765 TGC CCA GCA CCT GAA GGC AGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT PAPEGRLKIAAFNI 855 846 837 828 819 GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG S N A T L V I S Y M 900 909 891 882 873 AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC Y D I A L V Q E V R D S H L 954 963 972 945 936 927 GTG GAG AAG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC N Q D A L D N K L ${
m L}$ 1008 1017 999 990 GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG V V S E P L G R N S Y K E R Y L F V 1044 1053 1062 1071 1080 1035 TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC Y R P D Q V S A V D S Y Y D D G C 1089 1098 1107 1116 1125 1134 GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC E P C G N D T F N R E P A I V R F F 1143 1152 1161 1170 1179 1188 TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG S R F T E V R E F A I V P L H A A P 1197 1206 1215 1224 1233 1242 GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA G D A V A E I D A L Y D V Y L D V Q 1251 1260 1269 1278 1287 1296 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC E K W G L E D V M L M G D F N A G C 1305 1314 1323 1332 1341 1350 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC S Y V R P S Q W S S I R L W T S P T 1368 1377 1386 1395 1404 1359 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT F Q W L I P D S A D T T A T P T H C 1422 1431 1440 1449 1458 1413 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC A Y D R I V V A G M L L R G A V V P 1476 1485 1494 1503 1512 1467 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG DSALPFNFQAAYGLSDQL 1521 1530 1539 1548 1557 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' A Q A I S D H Y P V E V M L K *

in garage garage with

£ #

FIGURE 17

(A) pAS105

06-MAR-1995 PRI PAS105.DNA 1578 bp mRNA LOCUS Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS105) DEFINITION ACCESSION NID KEYWORDS DNase I. DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) Homo sapiens ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL 91067672 MEDLINE 442 g 310 t 473 c BASE COUNT 353 a ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT 1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA 1561 AAGAAGCGCA AGGTTTGA

- NLS

//

11.1



Figure 17(B)

```
25-AUG-2000
            FDDNASE105 1578 BP SS-DNA
                                                     SYN
CUS
FINITION
ACCESSION
MEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
                     /note="1 to 60 of 101/105linker"
                     join(721..>735,<736..>759,<760..>780)
     frag
                     /note="1 to 80 of 102linker [Split]"
                                            311 T
                                                       0 OTHER
                         471 C
                                   443 G
                353 A
BASE COUNT
ORIGIN
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
    301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
     361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
\mathbb{D}^{\mathbb{Z}}
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
       721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
       781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
       841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
       901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
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      1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
      1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
      1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
      1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
      1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
      1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
      1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
      1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
```

1561 AAGAAGCGCA AGGTTTGA

11

Figure 17k)

```
29-AUG-2000
                                                    SYN
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LOCUS
DEFINITION
ACCESSION
HEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     fraq
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     frag
                     /note="1 to 80 of 102linker [Split]"
                                           311 T
                                                       0 OTHER
                         477 C
                                  445 G
                354 A
BASE COUNT
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGCCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
      781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
      841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
       901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
       961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
      1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
      1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
      1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCGGGGGA CGCAGTAGCC
      1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
      1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
      1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
      1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
      1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
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1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGGGGGGC

1561 GGACCCAAAA AGAAGCGCAA GGTTTGA

.File: PAS105.DNA Range: 1 - 1578 Mode: Normal Codon Table: Universal

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FIGURE 17 (D)

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		9			18			27			36			45			54
ATG (GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
 М	 G	 W	S	C		I		- F	L	-	A	Т	A	Т	G	V	Н
		63			72			81			90			99			108
TCC	CAG		CAG	CTG						GAG	GTG	AAA	AAG	ССТ	GGG	GCC	TCA
 S	 Q	 V	 Q	 L	v	 Q	 S	G	 A	 E	 V	 K	к	-	 G	 А	
		440			100			125			1 // //			153			162
GTG	AAG	117 GTG	TCC	TGC	126 AAG			135 GGC							TGG	ATA	
- V	 К	- V	 S	 C	 K	 A	 S	 G	 Y	 T	 F	 S	 A	 Y		 I	E
		451			100			100			198			207			216
TGG	GTG	171 CGC		GCT	180 CCA		AAG	189 GGC		GAG			: GGA			ATT	
 W	 V	 R	 Q	A	P	 G	 K	 G	 L	 E	W	v	 G	E	 I	 L	P
		225			234			243			252	ļ		261			270
GGA	AGI						TAA	GAG	AAG	TTC	AAG	GGC	CGA	A GTG	ACA	GTC	ACT
-	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	Т	V	Т
		279	l		288	,		297			306	5		315	,		324
AGA	GAC	ACA	A TCC	C ACA	A AAC	ACA	GCC	TAC	ATC	GAG	G CTO	AGO	AGC	C CTC	AGC	TCT	GAG
R	Đ	T	S	т	N	T	A	Y	М	E	L	S	S	L	R	S	E
		333	3		342	2		351			360	O		369	7		378
GAC	ACA	A GCC	GT(C TA)AT 1	TGT	r GC <i>I</i>	A AGA	TC(TA:	C GA	C TT'	T GC	C TG(TT1	r GCT	TAC
D	$^{-}$ T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
		38															
TGC	GG 	C CA.	A GG 	G AC	T CT(G GT(C AC	A GT(TC(C TC 	A GC 	C TC 	C AC	C AA	G GG(C CCA	
W	G	Q	G	T	L	V	T	V	S	S	A	S	Т	K	G	P	S
		44			45			45			46				7		486
GT(TT	C CC 	C CT	'G GC 	:A CC	C TC	C TC 		G AG 		C TC	T GC 	G GG 		A GC	G GC(
V	F	, E	L	. A	ı P	S	S	K	S	J	: S	5 6	5 G	T	, Y	А	L
		49			50			51				2		53			54
GG(C TO	SC CI	`G G'I	TC AA	AG GA	.C TA	.C TT	'C CC	C GA 	.A C(CG G1 	.G A(CG G1	rg to 	:G TG	G AA:	C TC
G	(C I	. <i>\</i>	J I	ζ [) Y	F	, P	E	E I	. · · ·	7 5	r v	J S	S 1/2	I N	S
			i 9		55							76		5.8			59
GG	C G(CC CT	rg a	CC A	GC GC	SC GT	rg ca	AC AC	C T7	rc c(CG G(CT G'	rc co	ra ca	AG TC	C TC	A GG
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612 621 630 639 648 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG s v L Y S L S 675 684 693 702 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAA H K P S N T K V D K K T Y I C N V N 729 738 747 756 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT PKSCDKTHTCPPAP 774 783 792 801 765 GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG E G G L K I A A F N I Q T F G 855 837 846 828 819 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC S N A T L V S Y I V Q I L S 909 918 900 891 882 873 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG I A L V Q E V R D S H L T A V G K L 945 954 963 972 927 936 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG D N L N Q D A P D T Y Н L 999 1008 1017 1026 990 981 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC PLGRNSYKERYLFVYRPD 1035 1044 1053 1062 1071 1080 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG Q V S A V D S Y Y Y D D G C E P C G 1089 1098 1107 1116 1125 1134 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA N D T F N R E P A I V R F F S R F T 1143 1152 1161 1170 1179 1188 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V 1197 1206 1215 1224 1233 1242 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC A E I D A L Y D V Y L D V 1260 1269 1278 1287 1296 1251 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA L E D V M L M G D F N A G C S Y V R 1305 1314 1323 1332 1341 1350 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG PSQWSSIRLWTSPTFQWL 1368 1377 1386 1395 1359 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R 1422 1431 1440 1449 1413 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT I V V A G M L L R G A V V P D S A L 1476 1485 1494 1503 1512 1467 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC PFNFQAAYGLSDQLAQAI 1530 1539 1548 1557 1566 1521 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG D H Y P V E V M L K G G G P K K K

1575
CGC AAG GTT TGA 3'
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FIGURE 18

(A) pAS106

PRI 06-MAR-1995 PAS106.DNA 1596 bp mRNA LOCUS Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS106) DEFINITION ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) Homo sapiens ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL 91067672 MEDLINE 452 g 314 t 475 c 355 a BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC 1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG 1561 AAGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

lo NLS

Figure 12(B)

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25-AUG-2000
                                                    SYN
                       1596 BP SS-DNA
           FDDNASE106
CUS
FINITION
CESSION
FEYWORDS
COURCE
HATURES
                     Location/Qualifiers
                     join(1..>720,<799..1596)
     fraq
                     /note="1 to 1596 of PAS106.dna [Split]"
                     721..798
     fraq
                     /note="1 to 78 of 102/106linker"
                                  452 G
                                           315 T
                                                      O OTHER
                         474 C
                355 A
BASE COUNT
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
    3 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
     :541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
      781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
      841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
      901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
      961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
     1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
     1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
     1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
     1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
     1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
     1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
     1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
     1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
     1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
```

1561 AAGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

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Figure 12(c)

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29-AUG-2000
                                                    SYN
                        1605 BP SS-DNA
            FDDNASE106
LOCUS
DEFINITION
ACCESSION
EFYWCRDS
SOURCE
                     Location/Qualifiers
FEATURES
                     10..1605
     fraq
                     /note="1 to 1596 of FdDNase106correct"
                     join(10..>729,<808..1605)
     frag
                     /note="1 to 1596 of PAS106.dna [Split]"
                     730..807
     frag
                     /note="1 to 78 of 102/106linker"
                                            315 T
                                                       0 OTHER
                         480 C
                                  454 G
                356 A
BASE COUNT
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
     481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
       601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
       661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
       721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
       781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
       841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
       901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
       961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
      1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
      1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
      1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC
      1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
      1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
      1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
      1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
      1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
      1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
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1561 GTGATGCTGA AGGGGGGGGG ACCCAAAAAG AAGCGCAAGG TTTGA

'File: PAS106.DNA Range: 1 - 1596 Mode: Normal Codon Table: Universal

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FIGURE 18(D.)

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ATG (GGA	9 TGG	AGC	TO	T A	18 ATC												GGT	G:	rc c	:AC
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GTG	AAG	GTG																		. <u></u>	-
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TGG	GTG	CGC	: CA	.G G 	CT 	CCA	GGF		AG (
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		27				288															32
AGA	GA(C AC	A TO	CC A	ACA	AAC	AC	A G	CC	TAC	ATC	G GA 	G (CTC	A GC	AG(CT(G A0 	3G ' 	TCT 	GA
R	D	Т	•	S	T	N	Т		A	Y	M	E		L	S	S	L	F	ξ.	S	E
		33				342				351							36				37
GAC	AC	A GC	C G	TC	TAT 	TA(TG	T (GCA	AGA	TC(TA	. –	GAC	TT:	r GC 	C TG 	G T:	ГТ 	GCT	T' <i>F</i>
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		38					6				•						42				43
TG(G GG	SC CA	\A G	GG 	ACT	CT	G G:	rc . 	ACA	GTC	TC	C T(CA (GCC 	TC	C AC	C AA	.G G	GC 	CCA	T(
W	C	\$ Ç)	G	Т	L	7	J	\mathbf{T}	V	S		S	A	S	Γ	' k	(G	Р	:
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GT	C Ti	rc co	cc c	CTG	GCA	A CC	C T	CC 	TCC	AA(G AG	C A	CC 	TCT	' GG	G GG	SC A(CA G 	CG 	GCC	: C
V		: F :	 P	L	A	F)	S	S	K	S	5	T	S	G	; (3 5	r	А	А	
			95								3										
GG 	C T	GC C	TG (GTC	AA 	G G <i>I</i>	AC T	AC	TTC	CC	C G# 	\A С 	CG 	GT(G AC	CG G	rg T 	UG 1 	.'GG 	AA(. T
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612 621 630 639 648 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG T V P S S S L Y S L S S V 684 693 702 675 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P K S N 720 729 738 747 756 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG K T H T C C V E K S C D 774 783 792 801 765 TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG PEGSGGLKIAAF 855 837 846 828 819 ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG T K M S N A T L V 918 909 900 882 891 873 ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG Y D I A L V Q E V R D S 972 963 954 945 936 927 ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT V G K L L D N L N Q D A P D 1026 1017 1008 999 990 981 CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG H Y V V S E P L G R N S Y K E R Y L 1035 1044 1053 1062 1071 1080 TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT --- --- --- --- --- --- --- --- --- --- --- ---F V Y R P D Q V S A V D S Y Y D D 1089 1098 1107 1116 1125 1134 GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG G C E P C G N D T F N R E P A I V R 1143 1152 1161 1170 1179 TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG F F S R F T E V R E F A I V P L H A 1197 1206 1215 1224 1233 1242 GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT A P G D A V A E I D A L Y D V Y L D 1251 1260 1269 1278 1287 1296 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG V Q E K W G L E D V M L M G D F N A 1305 1314 1323 1332 1341 1350 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC G C S Y V R P S Q W S S I R L W T S 1359 1368 1377 1386 1395 1404 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG PTFOWLIPDSADTTATPT 1422 1431 1440 1449 1458 1413 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT H C A Y D R I V V A G M L L R G A V 1467 1476 1485 1494 1503 1512 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC V P D S A L P F N F Q A A Y G L S D 1530 1539 1548 1557 1566 1521 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG Q L A Q A I S D H Y P V E V M L K G 1575 1584 1593 GGC GGA CCC AAA AAG AAG CGC AAG GTT TGA 3' Р К K K R K V *

11

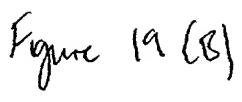
FIGURE 19

(A) pAS107

1590 bp PRI LOCUS PAS107.DNA mRNA 06-MAR-1995 Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS107) DEFINITION ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL MEDLINE 91067672 BASE COUNT 474 c 448 g 354 a 314 t ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC 1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG 1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

LONLS



```
1590 BP SS-DNA
            FDDNASE107
                                                     SYN
                                                               25-AUG-2000
J.OCUS
TFINITION
CESSION
MAYWORDS
SOURCE
                     Location/Qualifiers
FFATURES
                     join(1...>720,<793..1590)
     frag
                     /note="1 to 1590 of PAS107.dna [Split]"
                     721..792
     fraq
                     /note="1 to 72 of 103/107linker"
                     join(721..>771,<772..792)
     fraq
                     /note="1 to 78 of 102linker [Split]"
                         473 C
                                  448 G
                                           315 T
BASE COUNT
                354 A
                                                       0 OTHER
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
\mathcal{A}_{i}
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
```

1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

Figure 19 (C)

```
29-AUG-2000
                                                     SYN
                        1599 BP SS-DNA
            FDDNASE107
1.0CUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
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     frag
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                     join(730..>780,<781..801)
     frag
                     /note="1 to 78 of 102linker [Split]"
                                   450 G
                                                       0 OTHER
                          479 C
                                            315 T
                355 A
BASE COUNT
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGCCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
<u>LO</u>V
     241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
1. . . .
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
80
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
       601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
       661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
       721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
       781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT
       841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
       901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
       961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
      1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
      1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
      1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
      1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
      1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
      1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
      1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
      1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
      1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
      1561 CTGAAGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA
```

File: PAS107.DNA
Range: 1 - 1590
Codon Table: Universal Mode : Normal

FIGURE 19 (0)

		9			18			27			36			45			54
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
 М	G	W	S	С	I	I	L	F	L	V	A	T	А	T	G	V	H
		63			72			81			90			99			108
TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	ССТ	GGG	GCC	TCA
S	Q	V	Q	L	V	Q	S	G	Α	E	V	К	K	P	G	Α	S
		117			126			135			144			153			162
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GA(
V	K	V	S	С	K	A	S	G	Y	Т	F	S	A	Y	W	I	E
		171			180			189			198			207			21
TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	ATT	CC
W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
		225			234			243			252			261			27
GGA	AGT	AAT	AAT	TCT	AGA	TAC	TAA	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	AC'
G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	${f T}$	V	T
		279			288			297			306			315			32
AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GA
R	D	Т	S	Т	N	T	A	Y	М	E	L	S	S	L	R	S	E
		333			342			351			360			369			37
GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TA
a	т	А	V	Y	Y	C	A	R	S	Y	D	F	A	M	F	A	Y
		387			396			405						423			43
TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TC
W	G	Q	G	${f T}$	L	V	T	V	S	S	A	S	Т	K	G	Р	S
		441			450			459			468			477			48
GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CT
V	F	P	L	А	Р	S	S	K	S	Т	S	G	G	Τ	A	A	L
		495															54
GGC	C TGC	CTC	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTO	TC0	TGG	AAC	TC
G	С	L	V	K	D	Y	F	P	E	Р	V	Т	V	S	W	N	S
		549)		558			567	7		576	; •		585	>		59
GG(C GCC	CTC	ACC	AGC	GGC	GTC	G CAC	ACC	TTC	CCC	GCI	GTC	CTI	A CAC	TCC	TCA	s GG
G	A		т	S	G	V	⊸ ~ ~		 F		 h		 ¥	0		 S	. - .

-] -

621 630 639 648 612 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG V S S L Y S L 702 693 675 684 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA K V N H K P S N N 747 729 738 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG D K T H C K 810 792 801 783 774 765 TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT E G G L K I A A F N I Q 855 864 846 837 828 819 GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG K M S N A T L V S Y I V O 900 909 918 891 873 882 AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC E R \mathbf{D} V I A L V Q S Y D 954 963 972 945 936 927 GTG GGG AAG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC D A Р D Nm L N Q L 1008 1017 990 999 981 GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG V V S E P L G R N S Y K E R Y L F V 1035 1044 1053 1062 1071 1080 TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC Y R P D Q V S A V D S Y Y D D G C 1098 1107 1116 1125 1134 1089 GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC E P C G N D T F N R E P A I V R F F 1152 1161 1170 1179 1188 1143 TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG S R F T E V R E F A I V P L H A A P 1197 1206 1215 1224 1233 1242

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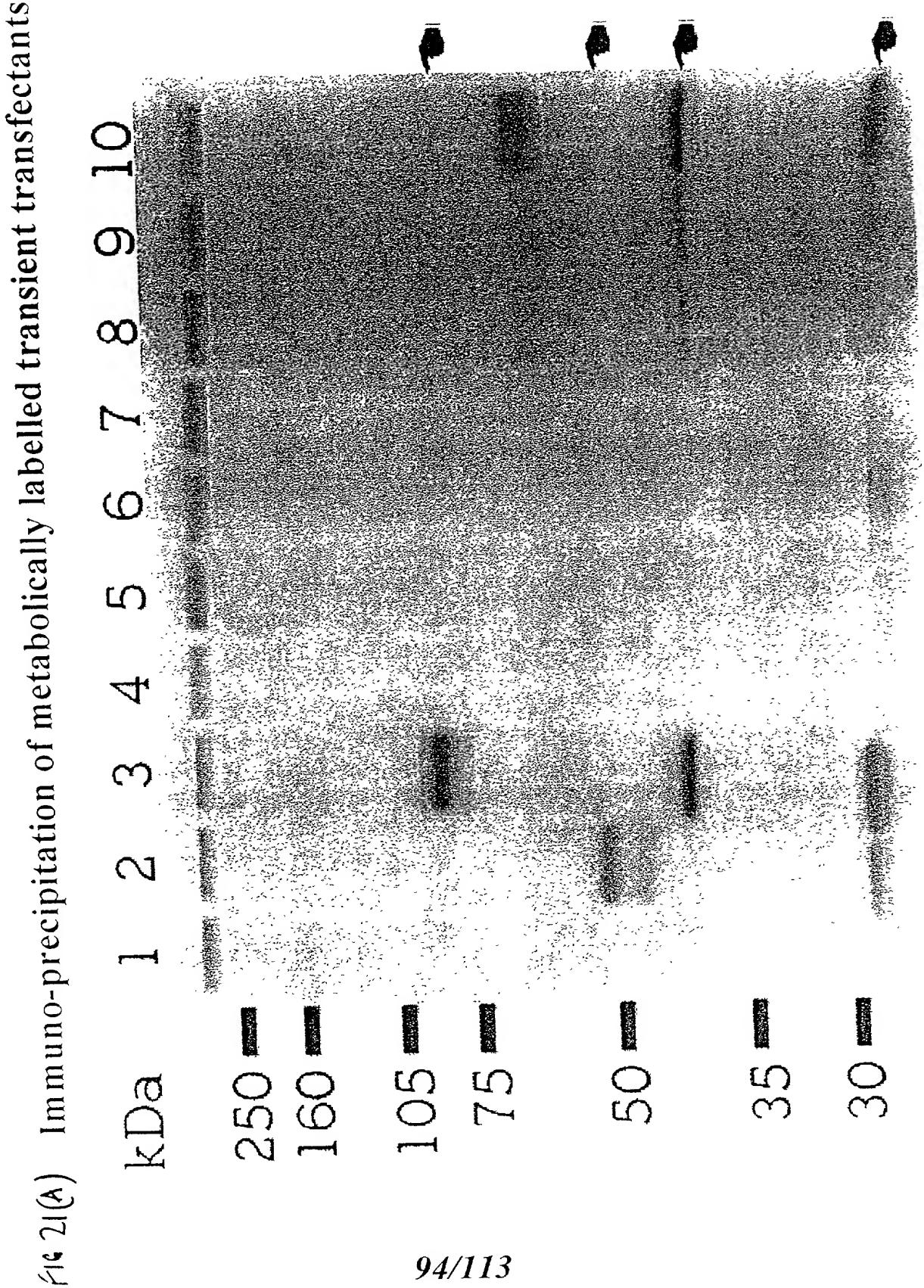
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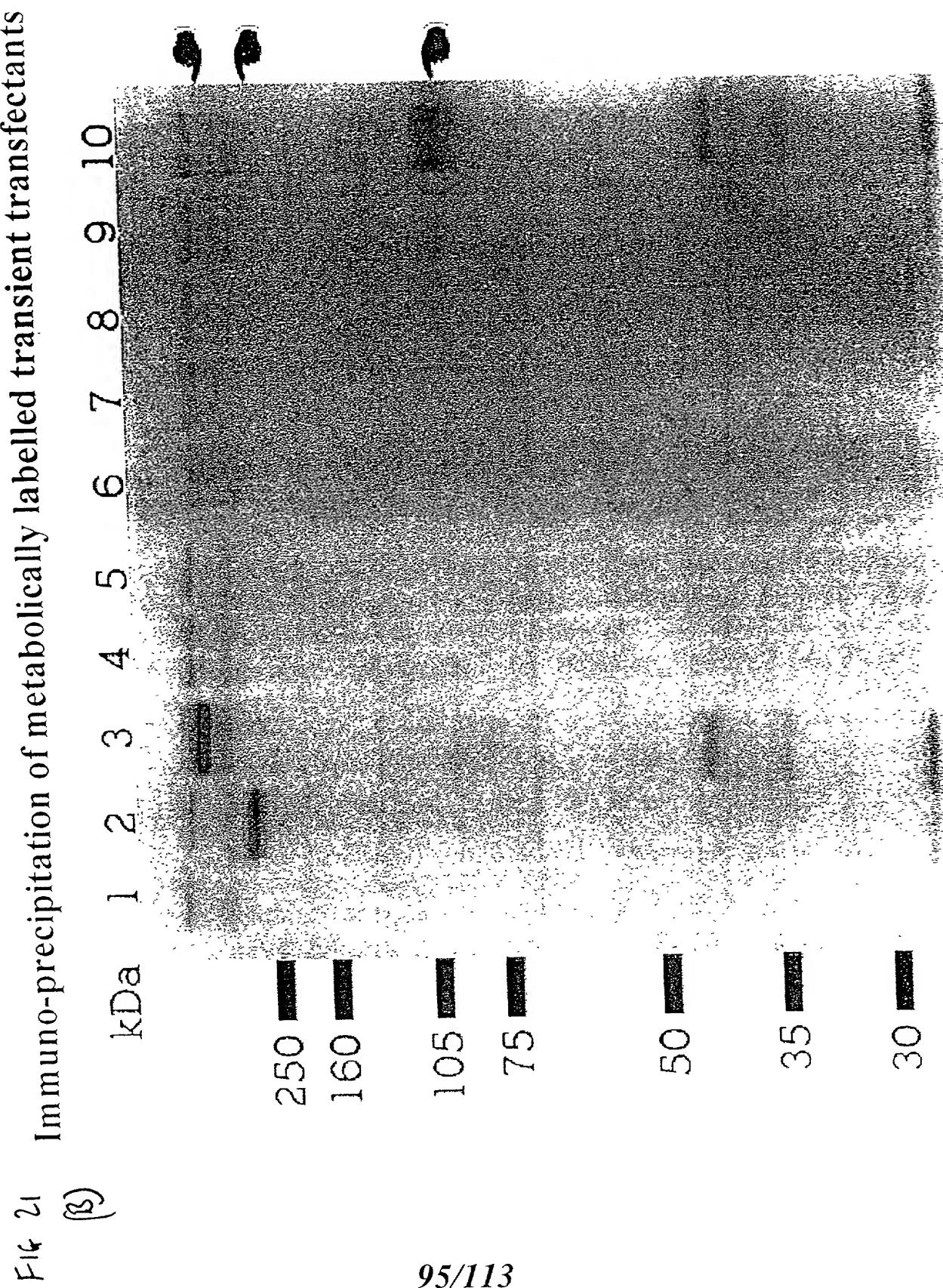
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GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA G D A V A E I D A L Y D V Y L D V Q 1251 1260 1269 1278 1287 1296 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC E K W G L E D V M L M G D F N A G C 1305 1314 1323 1332 1341 1350 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC S Y V R P S Q W S S I R L W T S P T 1359 1368 1377 1386 1395 1404 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT F Q W L I P D S A D T T A T P T H C 1413 1422 1431 1440 1449 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC A Y D R I V V A G M L L R G A V V P 1467 1476 1485 1494 1503 1512 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG DSALPFNFQAAYGLSDQL 1539 1548 1557 1566 1530 1521 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA A Q A I S D H Y P V E V M L K G G G 1584 1575 CCC AAA AAG AAG CGC AAG GTT TGA 3'

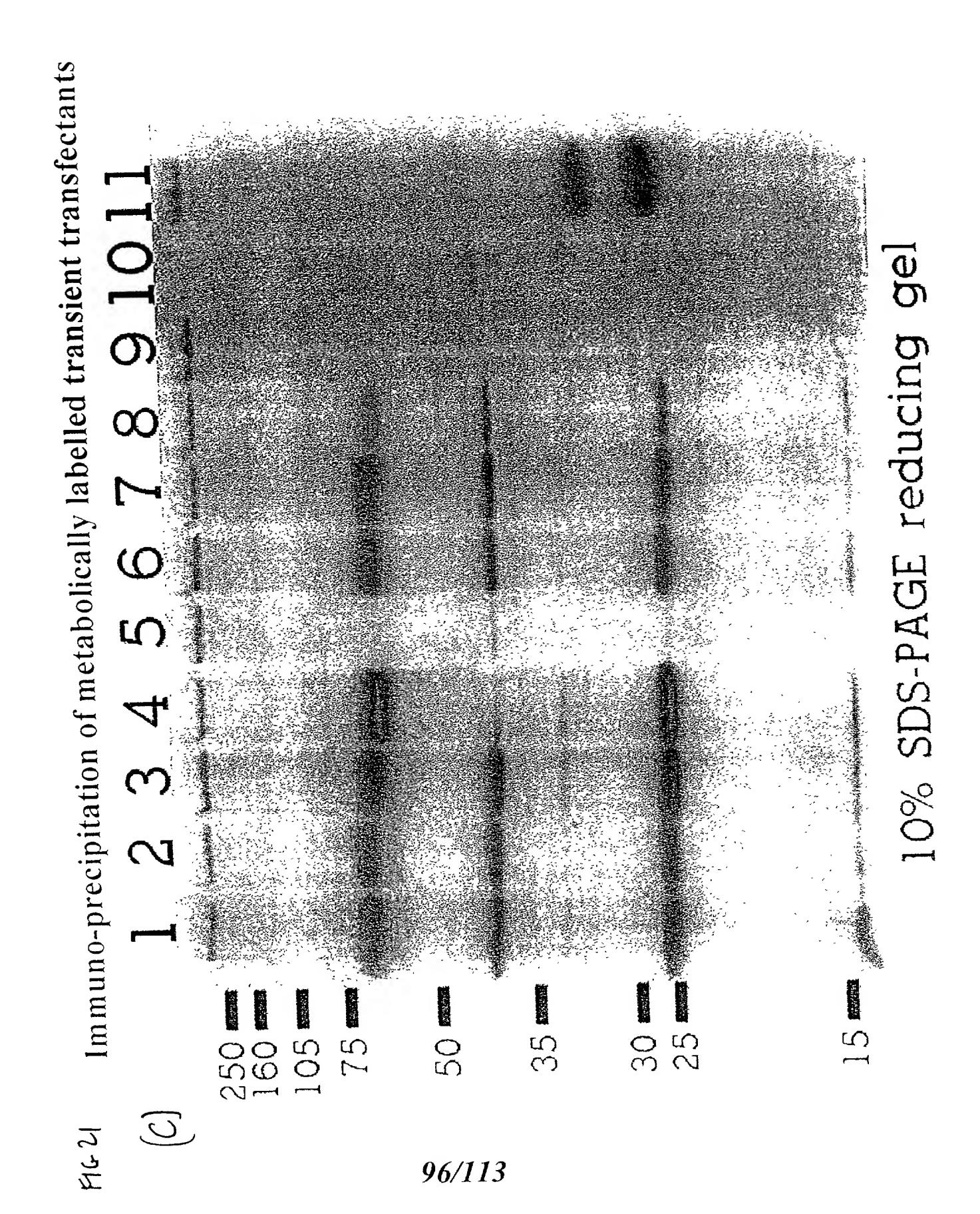
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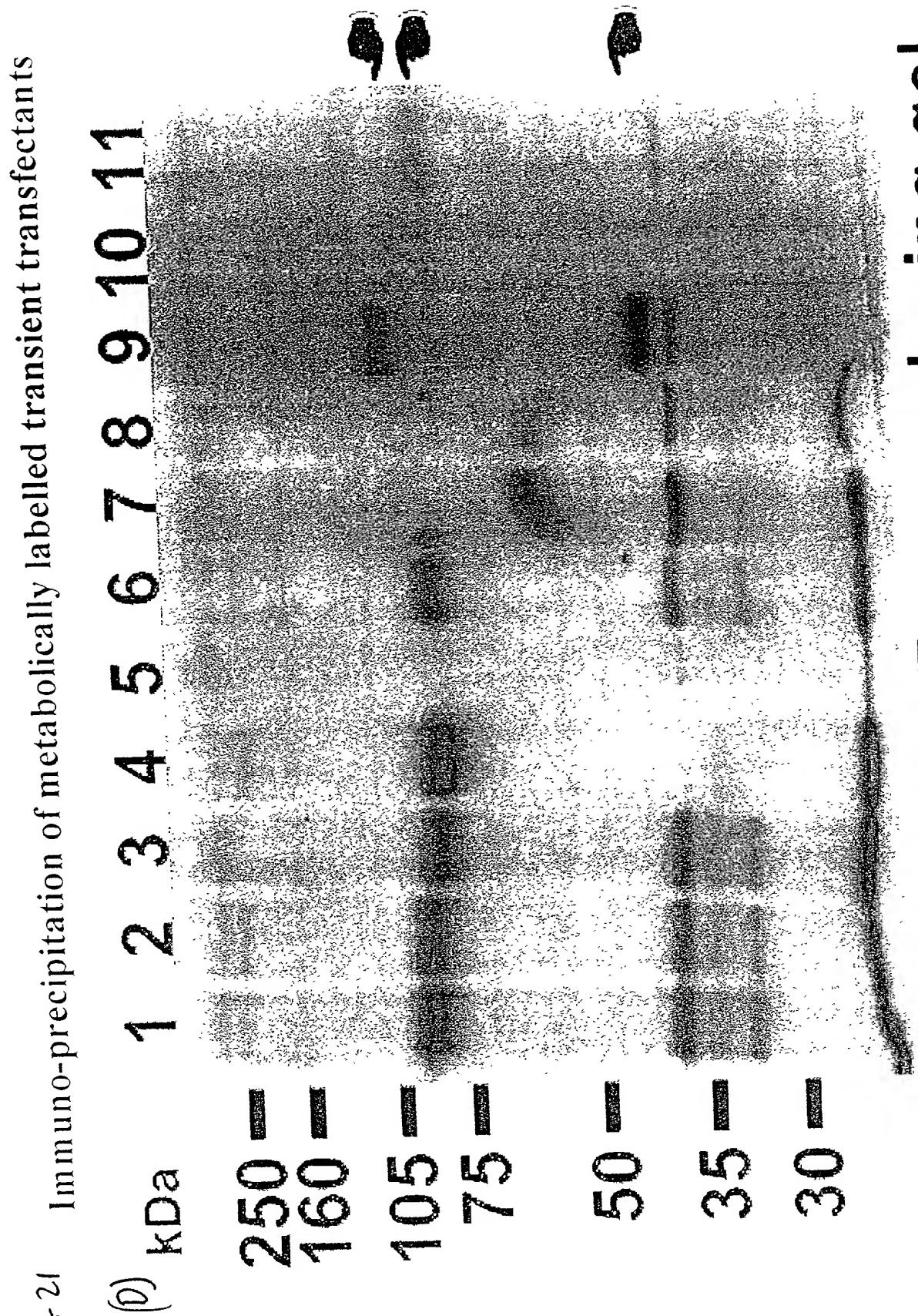
F19 20



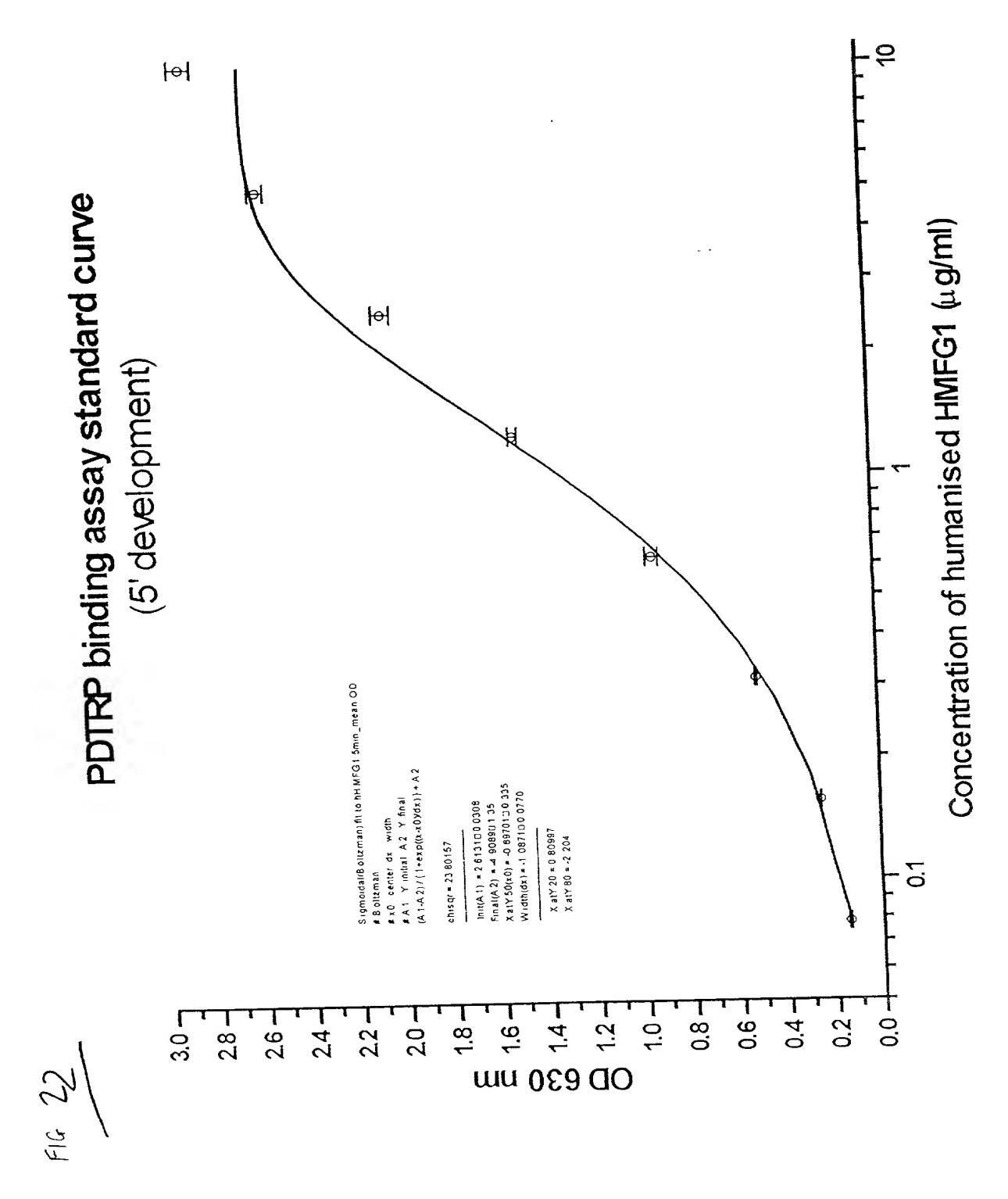


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Corrected bovine DNase I standard curves at various time points

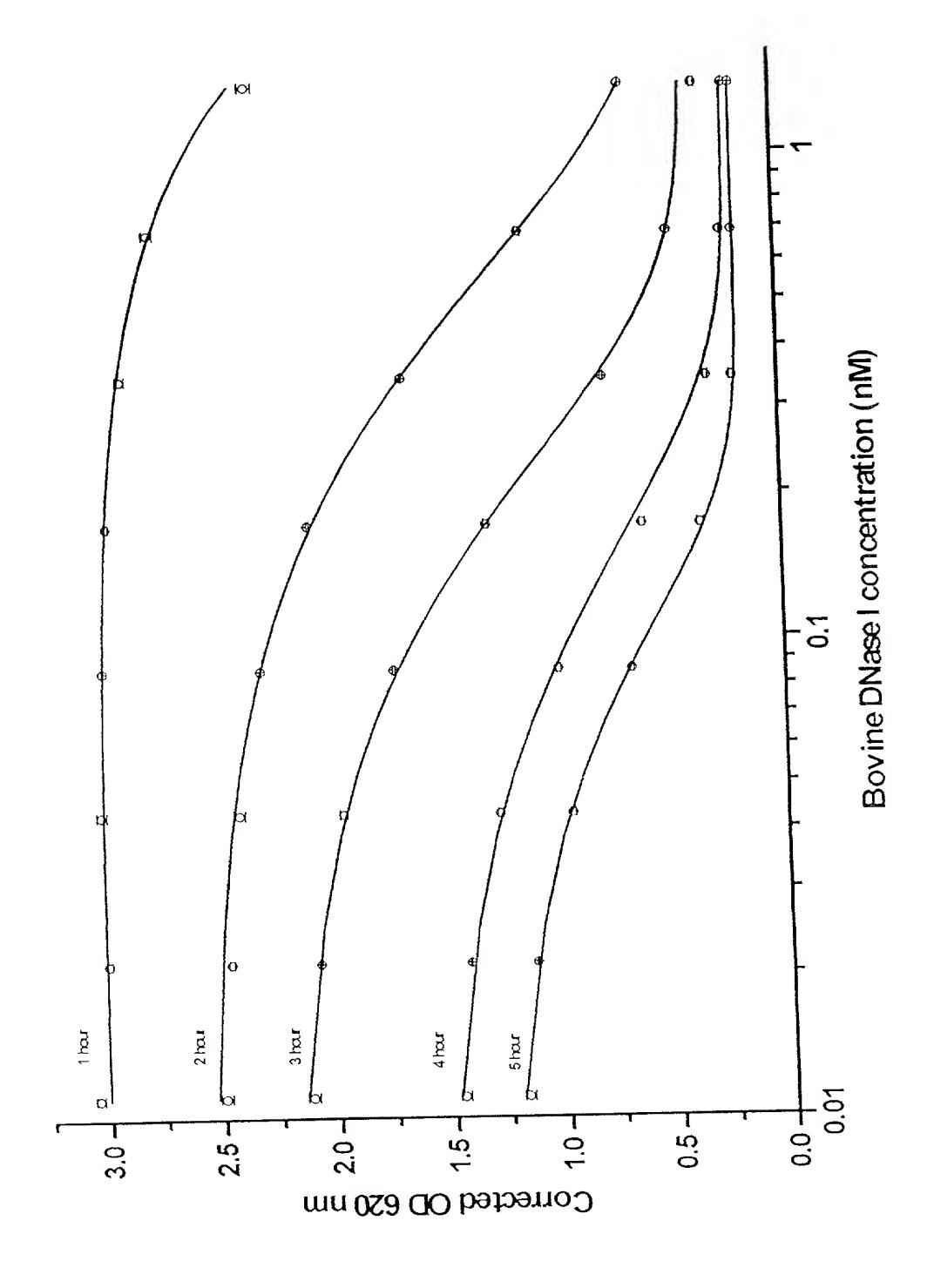
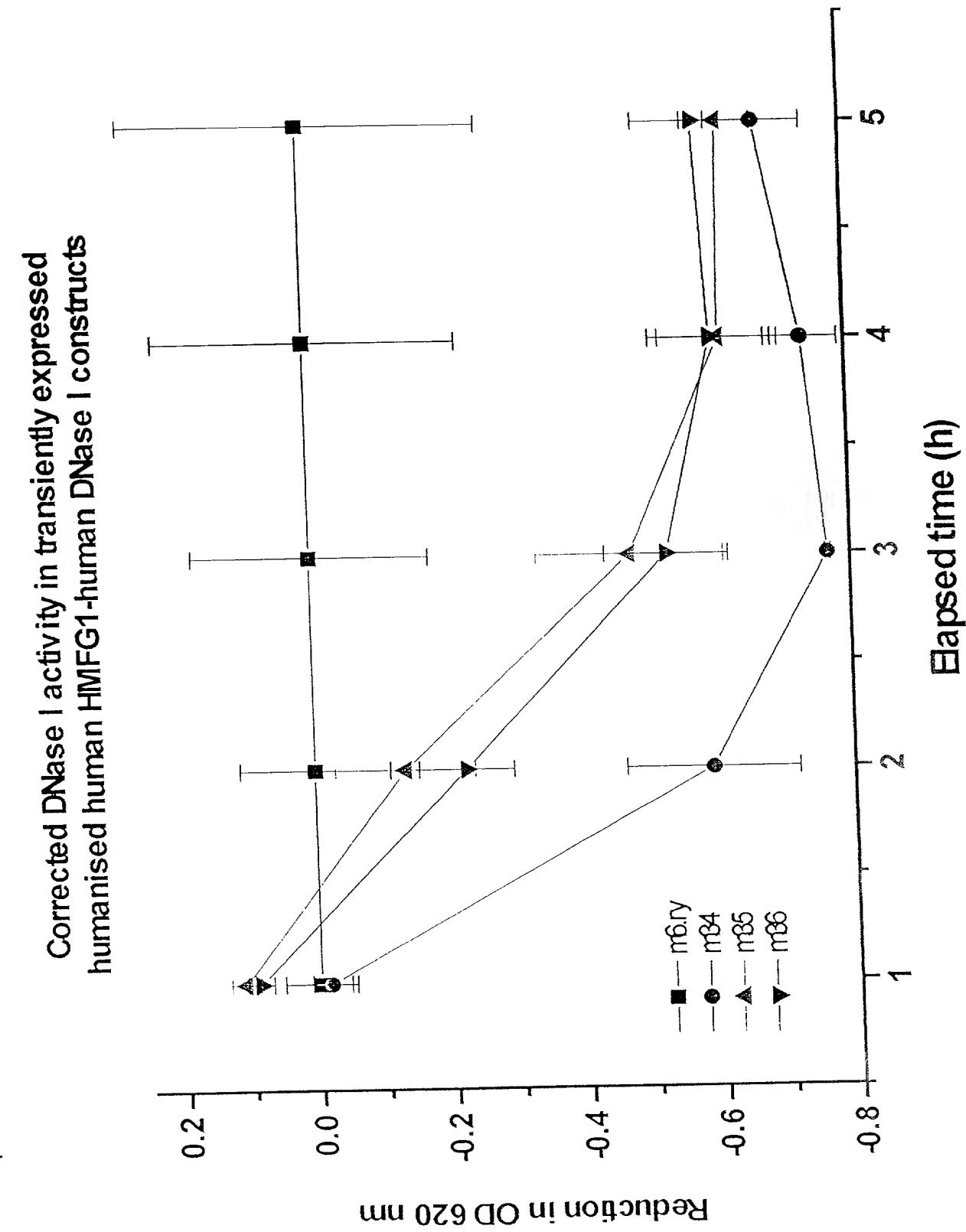


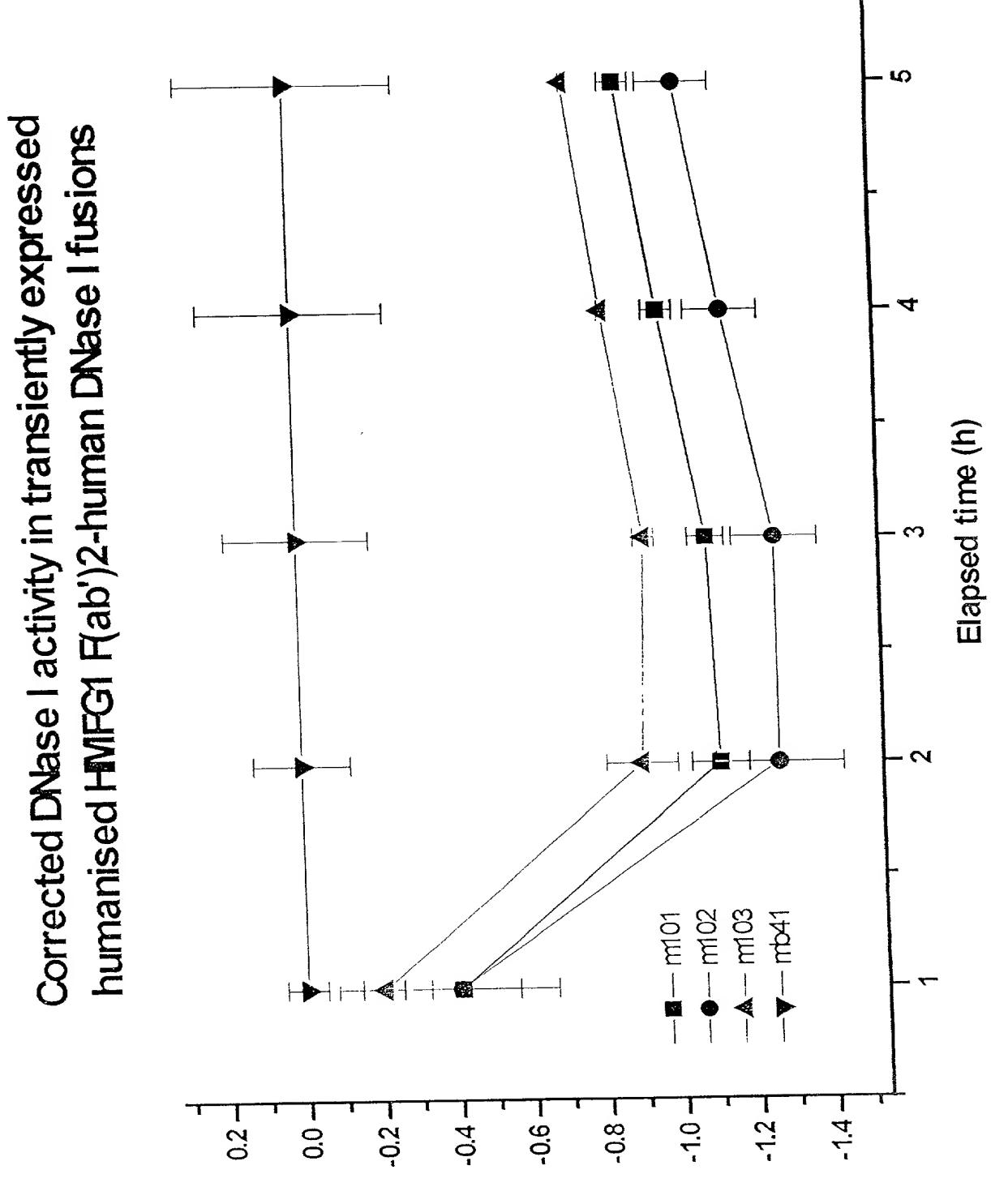
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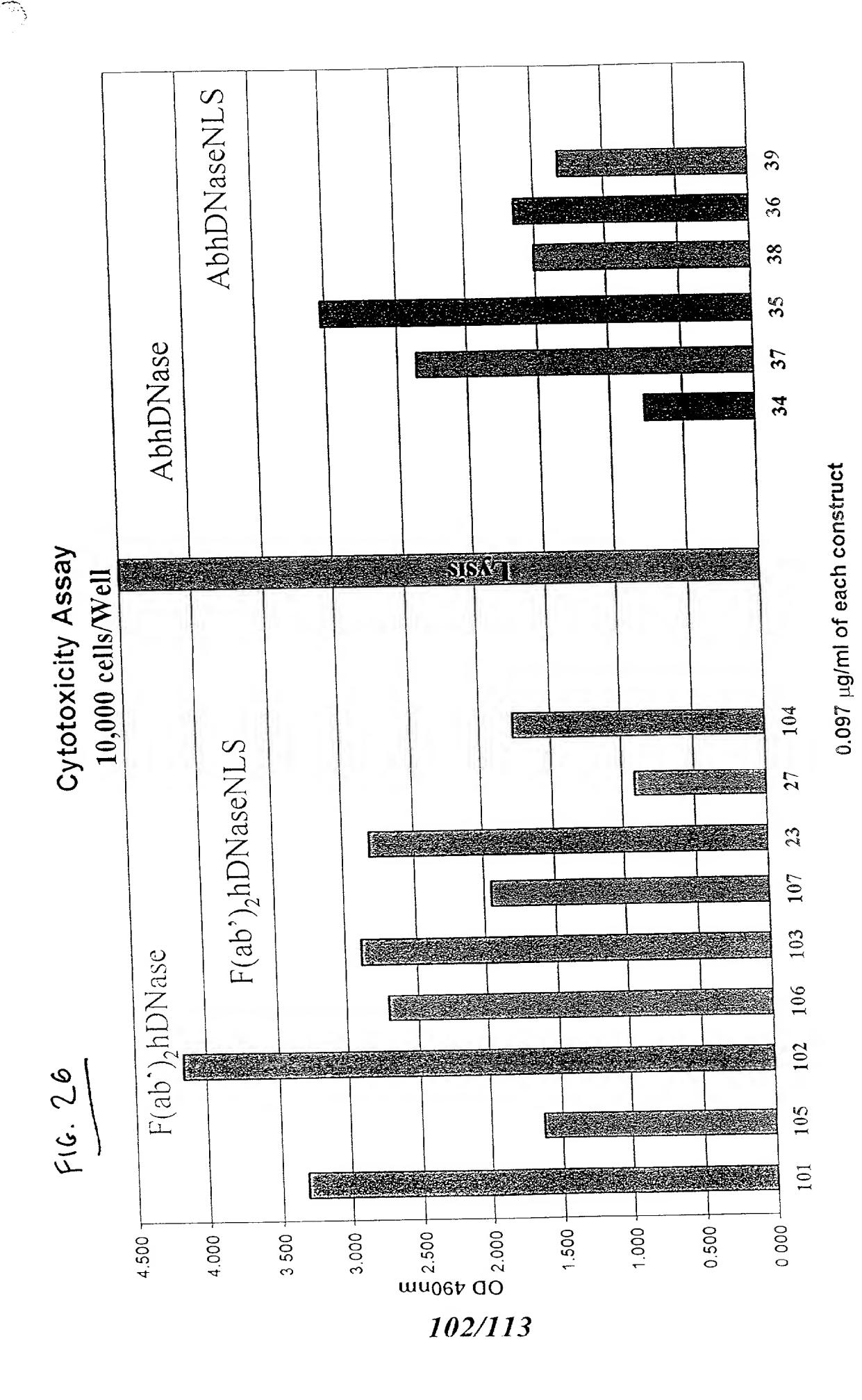
100/113



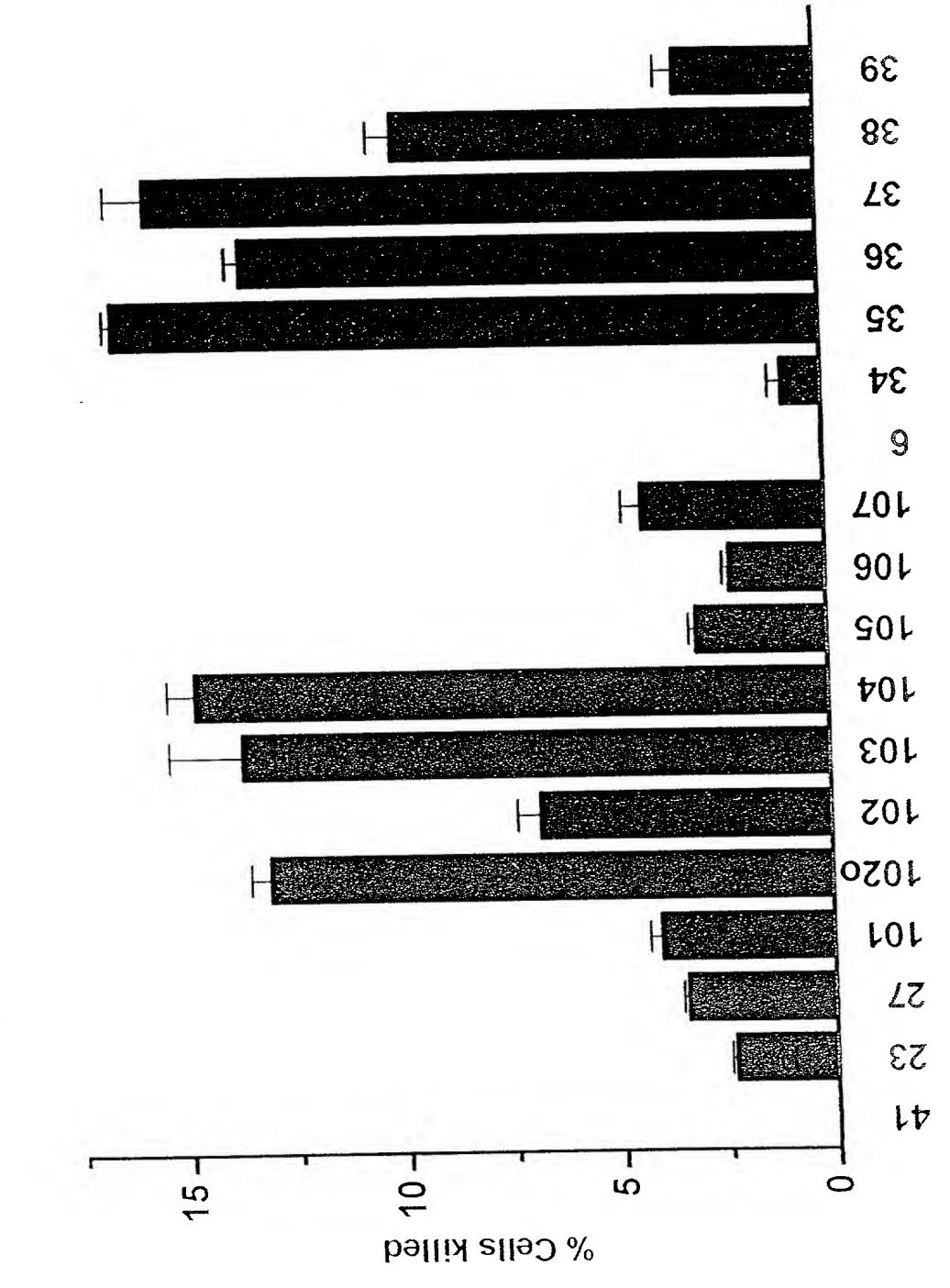
Reduction in OD 620 nm

101/113







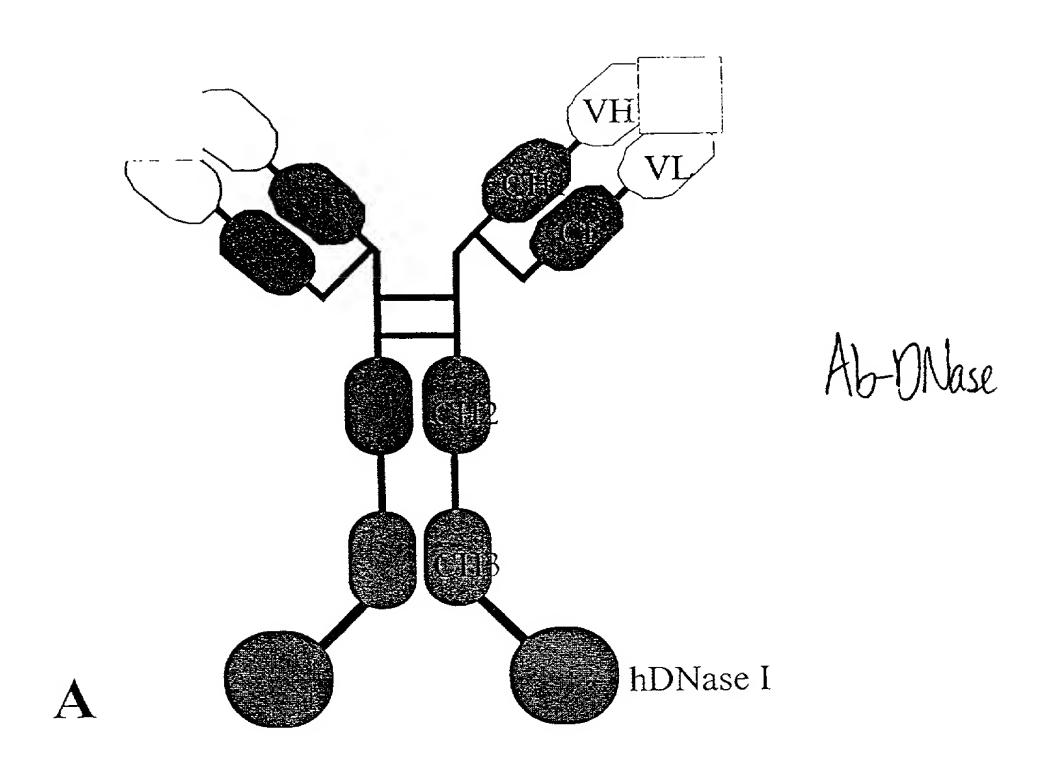


Construct number

F16 27

103/113

Figure 28



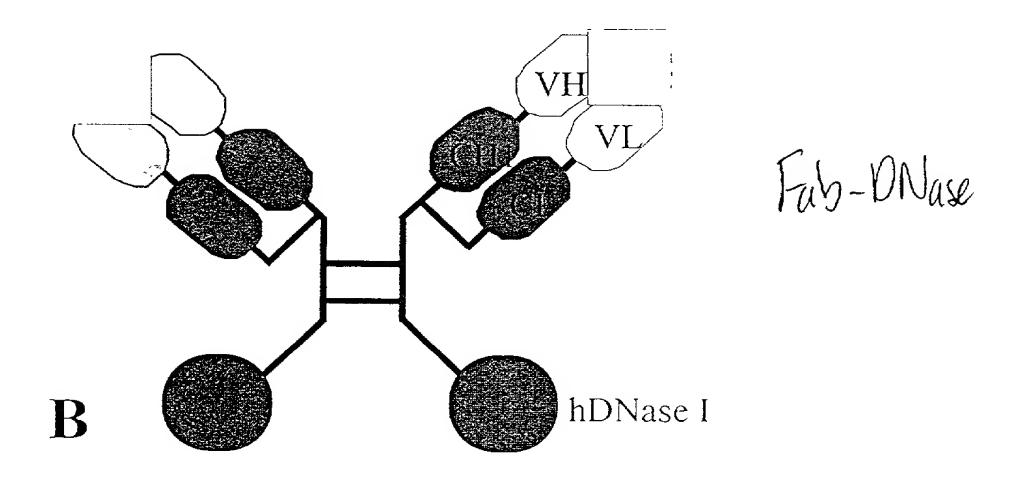
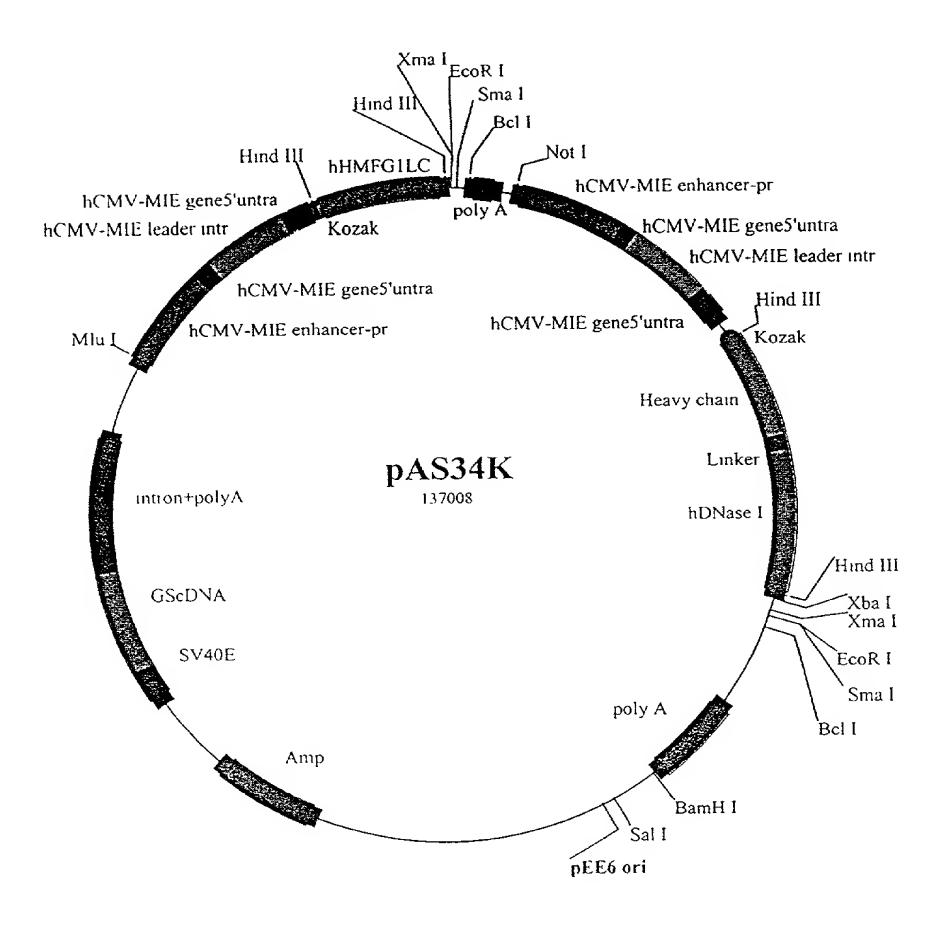
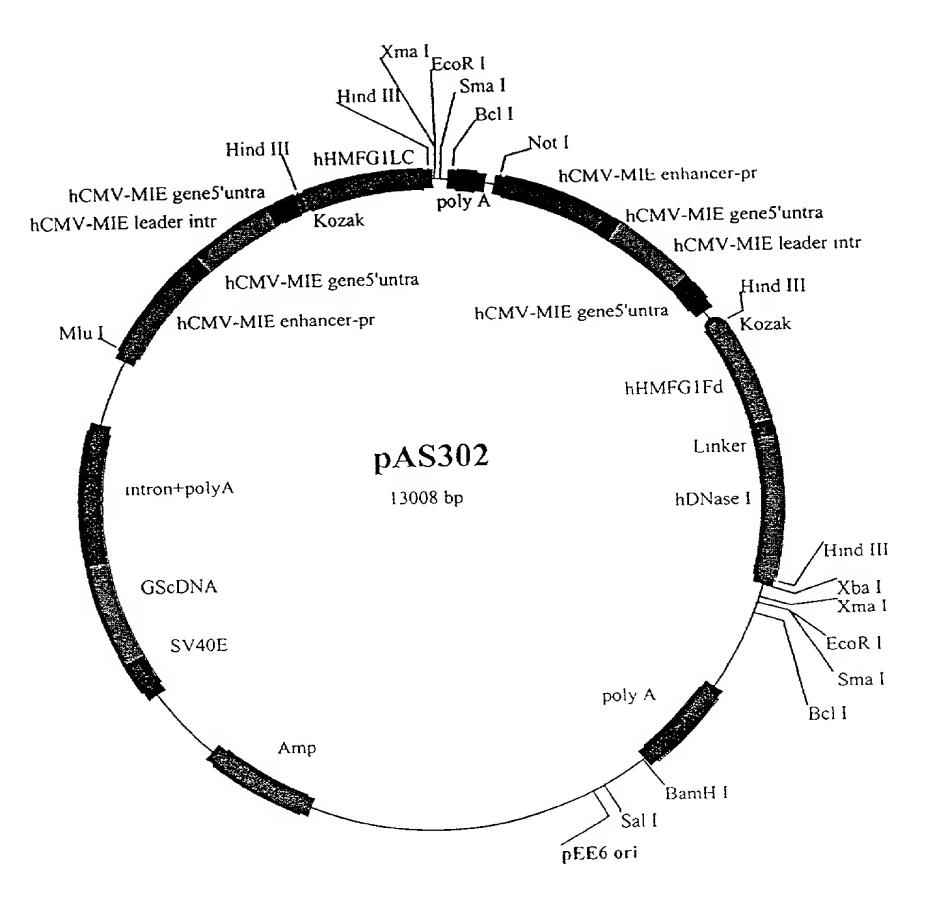


Figure 29



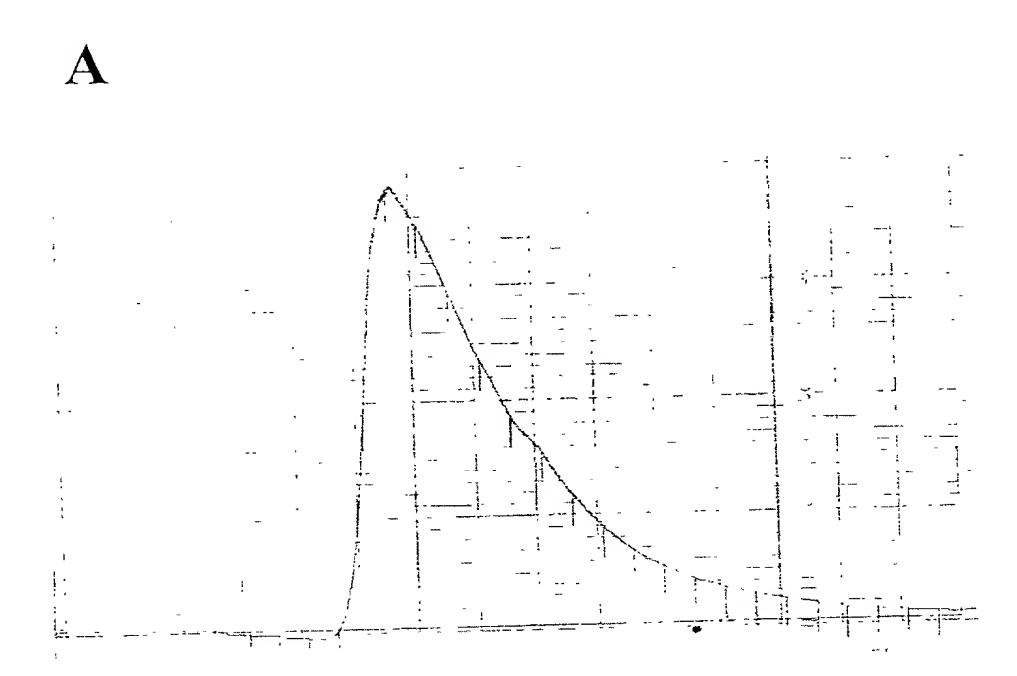
Ab-DNase

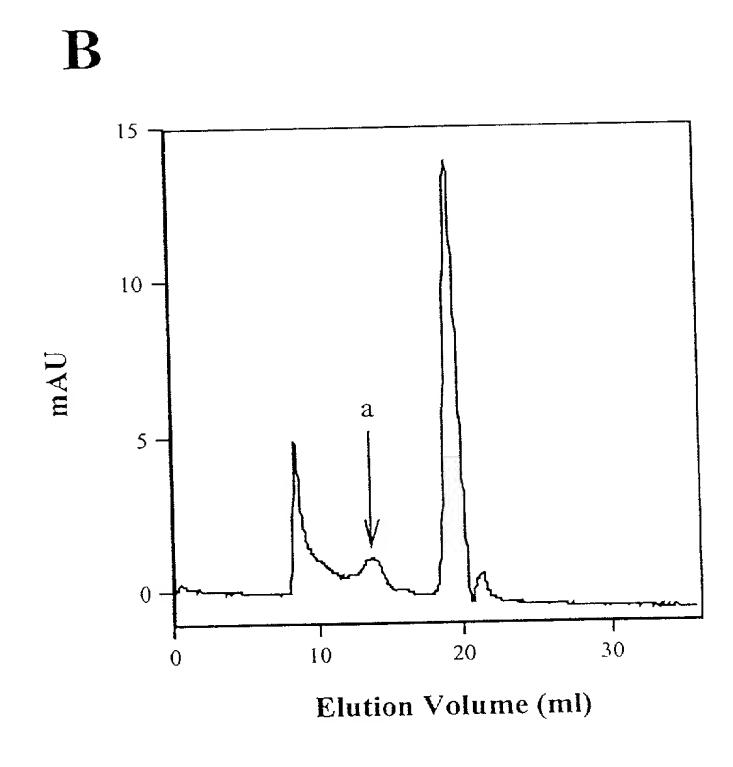
Figure 30



Fab-DNase

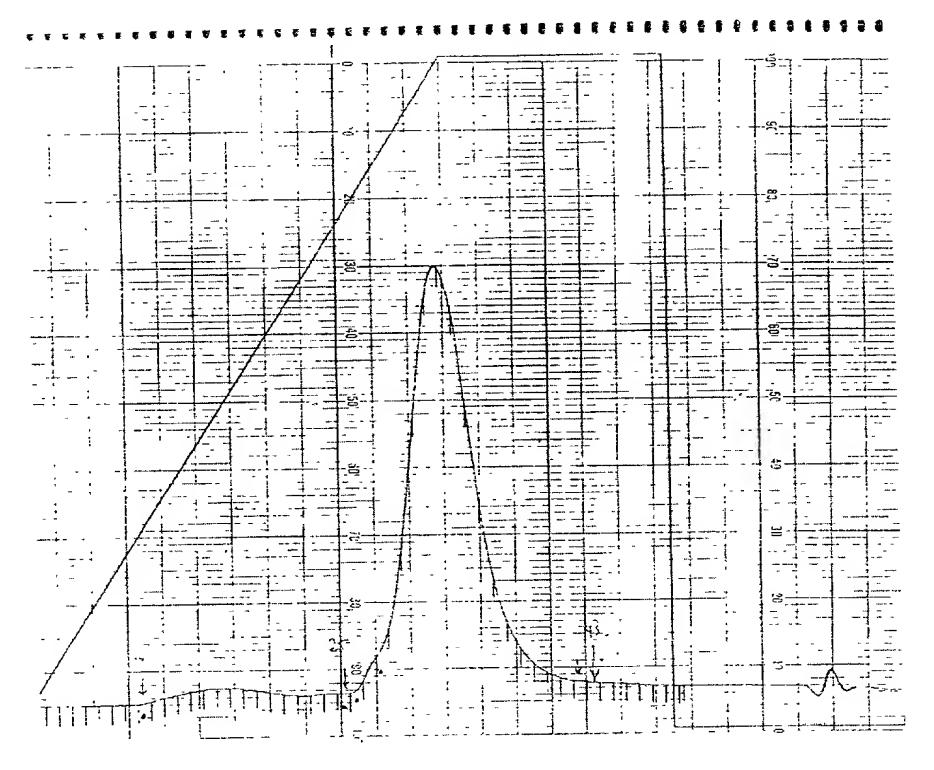
Figure 31



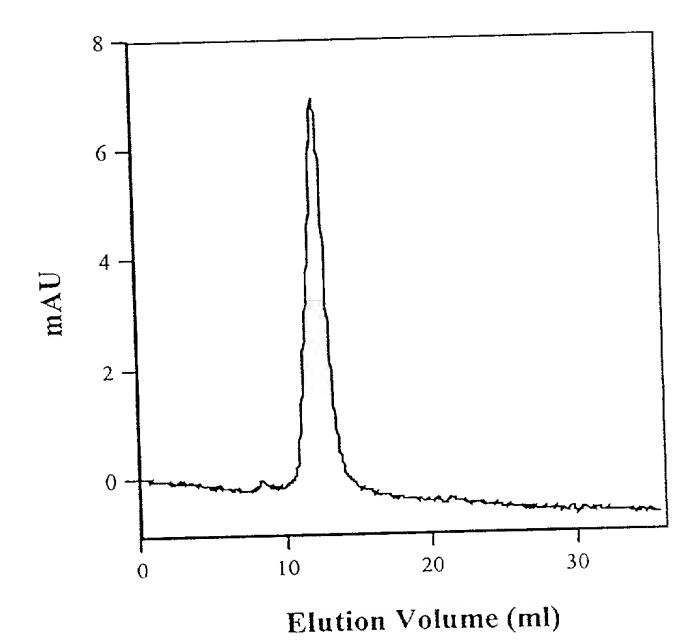


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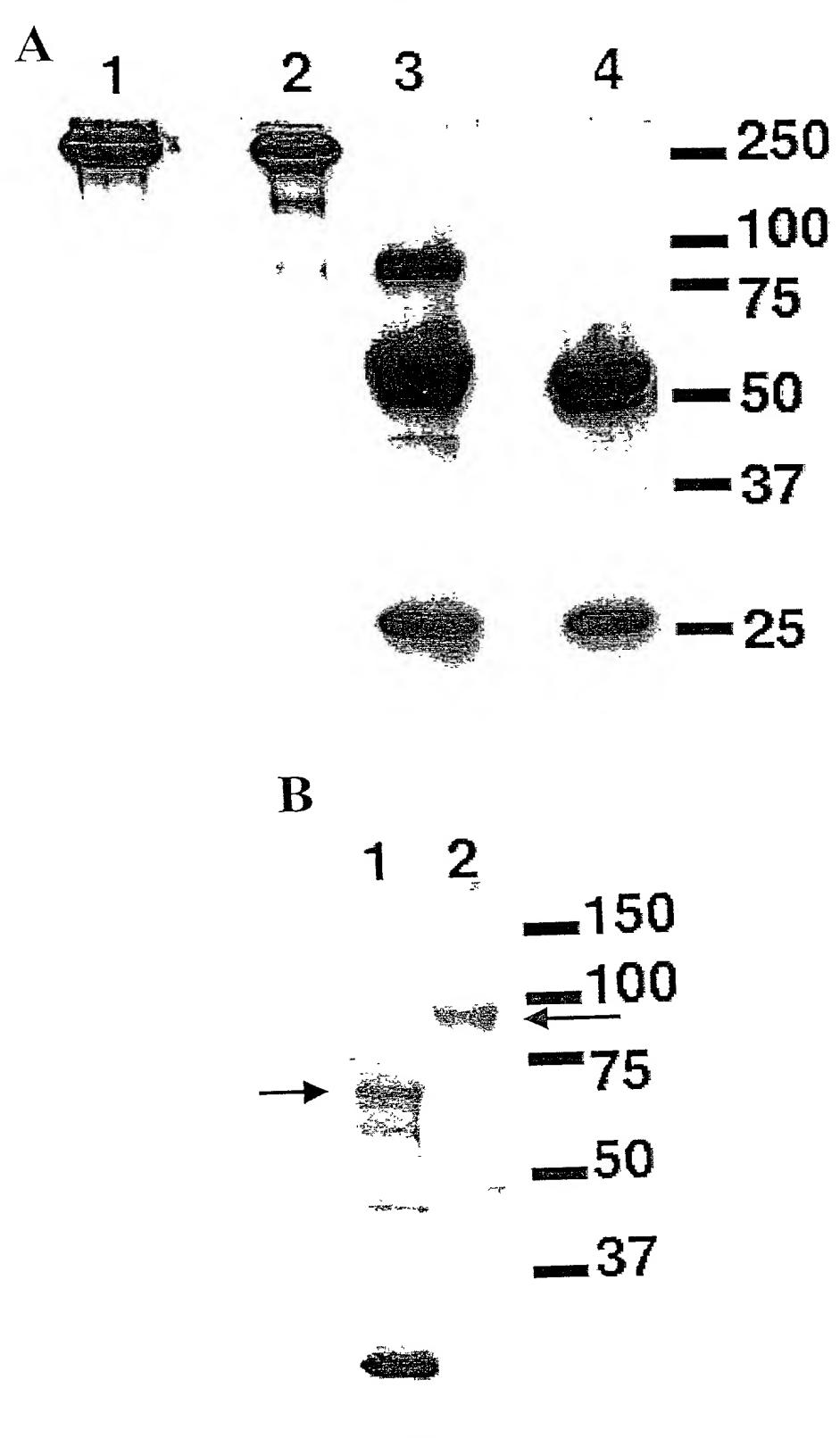


B



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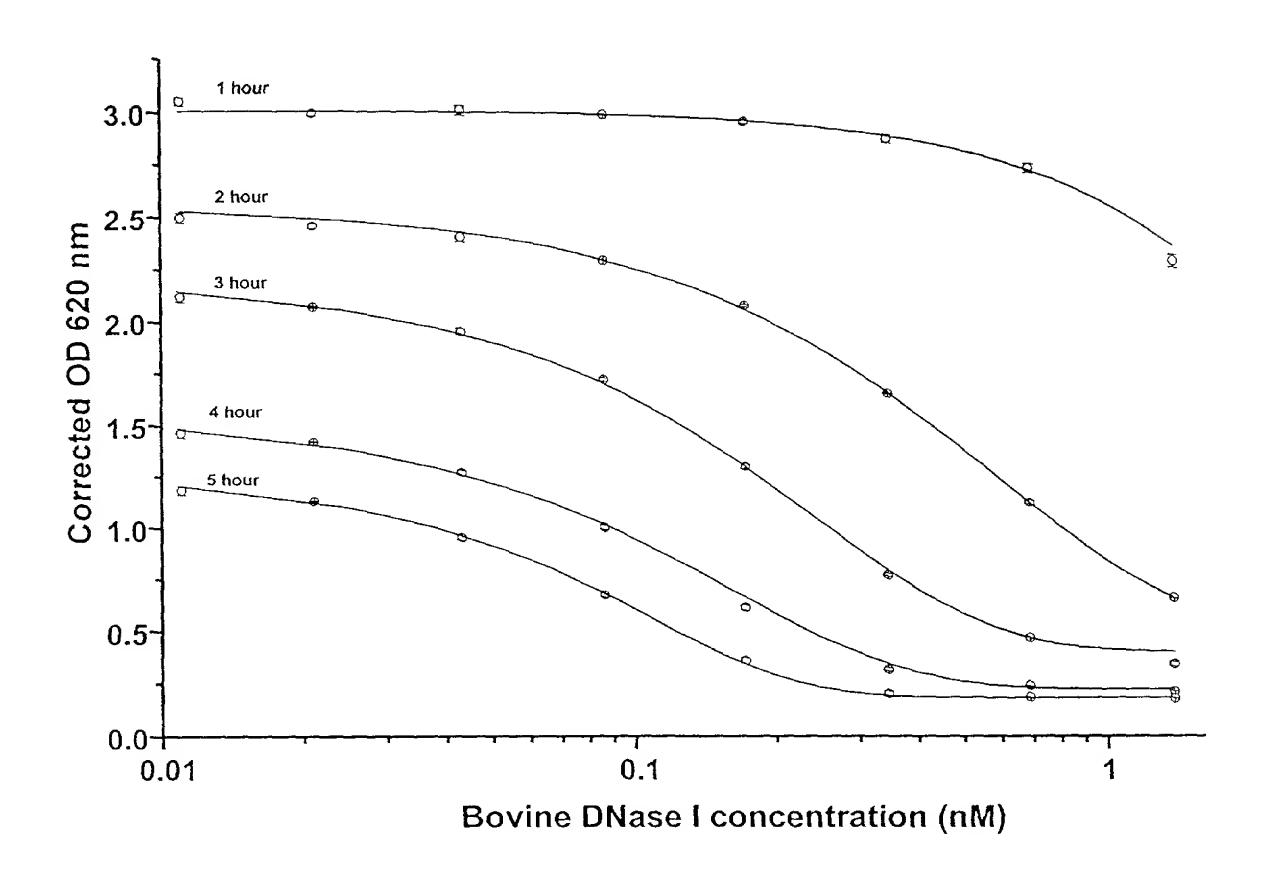
Figure 33



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Figure 34

Bovine DNase I standard curves at various time points



 ${\bf A}$

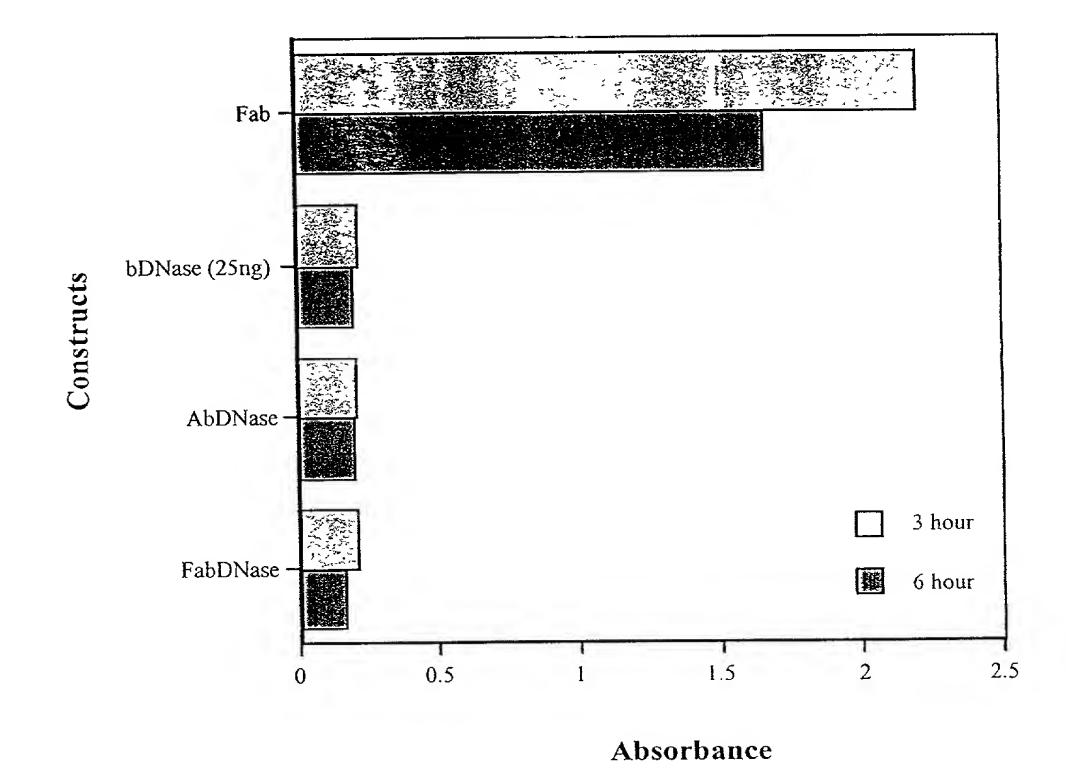


Figure 35

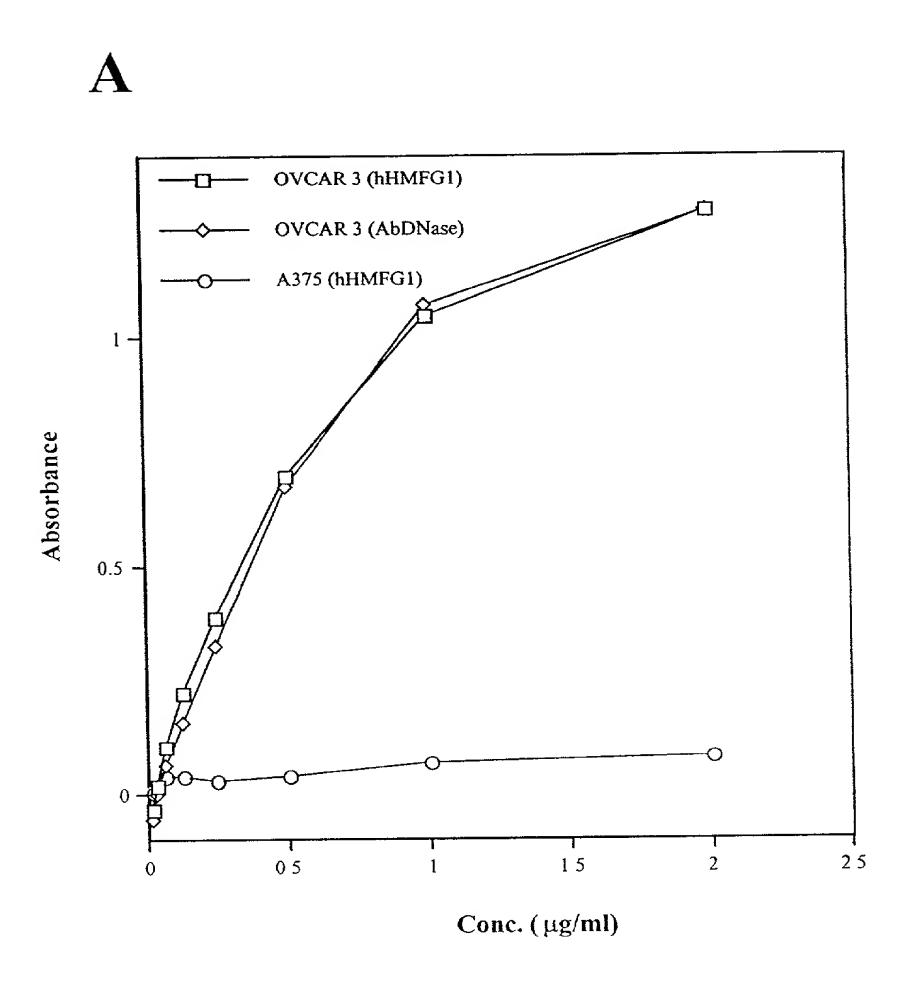


Figure 35 – cont.



